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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
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length: 2000000000
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1439
1 MVSAKDFSGAELYT1
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Gapop 10.0 , Gapext 0.5
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        MVSAKDFSGAELYTLEEVQY......PNSSSVDKLAAALEHHHHHH
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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US-09-286-690-10
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US-09-286-690-17
US-09-159-106-12
US-08-159-106-12
US-08-159-106-13
US-08-159-106-13
US-08-712-072C-4
US-08-712-072C-4
US-08-712-072C-3
US-08-712-072C-3
US-08-712-072C-3
US-09-262-653A-4
US-09-262-653A-4
US-09-262-653A-4
US-09-262-731-8
US-09-330-945-2
US-09-330-945-37
US-08-392-828C-37
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6 10 Appli
6 11 Appli
6 11 Appli
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Qy 2 VSAKDFSGAELYTLJEEVQYGKFEJ Db 25 VSAKDFSGAELYTLJEEVQYGKFEJ Db 25 VSAKDFSGAELYTLJEEVQYGKFEJ Qy 62 LGKNPGSFQSNIITGKAGAQKTSI Db 85 LGKNPGSFQSNIITGKAGAQKTSI Db 122 TEGGQVSNLITGTQGLRFNLWSSES QY 122 TEGGQVSNLTGTQGLRFNLWSSES QY 145 TEGGQVSNLTGTQGLRFNLWSSES Db 145 TEGGQVSNLTGTQGLRFNLWSSES QY 182 FTLDWTDNFDTFDGSRWGKGDWTI	SOFTWARE: PatentIn Ver. SEQ ID NO 12 LENGTH: 228 TYPE: PRT ORGANISM: Fibrobacter S-09-286-690-12 Ouery Match Best Local Similarity Matches 204; Conservat	NUMBER: 1999-04 1999-10 NUMBER: 1999-10 NUMBER: 1997-10	ESULT 1  5 -09 -12  Sequence 12, Application US  PALENT NO. 6103511  GENERAL INFORMATION:  APPLICANT: Ljungdahl, Lars  APPLICANT: Chen, Huizhong  THIE OF INFORMATION:	3 95.5 6.6 1582 4 95.5 6.6 1582 5 95.5 6.6 1582	6 102.5 7.1 1581 7 95.5 6.6 1581 9 95.5 6.6 1581 9 95.5 6.6 1581 0 95.5 6.6 1581 0 95.5 6.6 1581 2 95.5 6.6 1582	10.5 10.5 10.5 2.5 7.1 2.5 7.1 2.5 7.1
AKDFSGAELYTLJEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEV 61	genes Score 1103; DB 3; Length 228; Pred. No. 3.3e-105; O; Mismatches 0; Indels 0; Gaps 0	US/09/286,690 -05 US 60/027,882 -04 PCT/US97/17811	90	-08-476-900A-9 Sequence 9, Appl -08-488-546A-9 Sequence 9, Appl -08-726-320-5 Sequence 5, Appl ALIGNMENTS'	-09-208-716-3 Sequence 3, Appl -08-404-531B-6 Sequence 6, Appl -08-476-900A-6 Sequence 6, Appl -08-488-546A-6 Sequence 6, Appl -08-726-320-4 Sequence 4, Appl -09-208-716-4 Sequence 4, Appl -09-208-716-4 Sequence 9, Appl	37-2 Sequence 2, 72C-2 Sequence 2, 31B-3 Sequence 3, 00A-3 Sequence 3, 46A-3 Sequence 3, 20-1 Sequence 1, 50-3 Sequence 1, 50-1 Sequence 1, 50-1 Sequence 1,

US-09-286-690-8 ; Sequence 8, Application US/09286690 ; Patent No. 6103511 ; GENERAL INFORMATION:

APPLICANT: Ljungdahl, APPLICANT: Chen, Huiz TITLE OF INVENTION: L FILE REFERENCE: 55-96 APPLICANT: Li, Xin-Liang

Huizhong

Lars G.

Lichenase and Coding Sequences

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watches 59; Conserve
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US-08-103-998-2
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; SEQ ID NO 8
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-286-690-8
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COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Fl
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EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: PCT/US97/17811
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEO ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: APPLICANT: Borris
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                               APPLICATION NUMBER: US 07/773,652
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30307/123
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 VSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
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                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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TELEPHONE:
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VENTION: A Thermostable (1,3-1,4)-beta-Glucanase
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Thomsen, Karl Kristian
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GENERAL INFORMATION:

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RESULT 5
US-09-286-690-10
; Sequence 10, Application US/09286690
; Patent No. 6103511
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US-09-286-690-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 279
TYPE: PRT
ORGANISM: Clostridium thermocellum
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
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APPLICANT: Li, Xin-Liang
APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
TITLE OF INVENTION: Lichenase and Coding Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: US 60/027,882 EARLIER FILING DATE: 1999-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/286,690
CURRENT FILING DATE: 1999-04-05
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137
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                                                                                                                                                                                                                                                                      82 REYGGSYPYKSGEYRTKSFFGYGYYEVRMKAAKNVGIVSSFFTYTGPS---DNNPWDEID 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 SYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDIEFL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                           G
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                                                                                                                                                                                                                                                                                        KDFSGAELYTLEEVQ-----YGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVD 58
                                                                                                                                                          VRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---ATANIPSTPGKIMMNLWNGTGVDDWLGSYNGAN-PLYAEYDWV---KYT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKDTTKVQFNYYTNGVGGH---EKVISLGFDASKGFHTYAFDWQPGYIKWYVDG-VLKHT
                                                                                                                      VYR----GTRNIPVTPGKIMMNLWPGIGVDEWLGRYD-GRTPLQAEYEYVKYY
                                                                                                                                                                                              IEFLGKDTTKVQFNWYKNGVGG---NEYLHNLGFDASQDFHTYGFEWRPDYIDFYVDGKK 195
                                                                                                                                                                                                                                  IEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQE 118
                                                                                                                                                                                                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                                             Conservative
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35.5%;
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                                                                                                                                                                                                                                                                                                                                                            Score 231.5; DB 3
Pred. No. 9.1e-16;
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Pred. No. 3.8e-17;
                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                             DB 3;
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US-09-286-690-7
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                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver.
SEQ ID NO 7
LENGTH: 238
TYPE: PRT
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SEQ ID NO 10
LENGTH: 243
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                    Query Match
Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Lichenase and Coding Sequences FILE REFERENCE: 55-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chen, Huizhong
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APPLICANT: Ljungdahl, La:
APPLICANT: Chen, Huizhon
TITLE OF INVENTION: Lich
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                                         140 TKVQFNYYTNGVGGH---EKIINLGFDASTSFHTYAFDWQPGYIKWYVDG-VLKHT---A 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 ATTQIPQTPGK--IMMNLWNGAGVDEWLGSYN-GVTPLSRSLHWVRYTK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 GKDTTKVQFNYYTNGVG----NHEKIVNLGFDAANSYHTYAFDWQPNSIKWYVDGQ-LKHT 196
127 VSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 172
                                                                                     67
                                                                                                                               83
                                                                                                                                                                                                                                    Local Similarity
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                                                                               GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNKFDCGENRSVQTYGYGLYEVNMKPAKNVGTVSSFFTYTGPT---DGTPWDEIDIEFL 140
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                                                                                                                           FDCGEYRSTNNYGYGLYEVSMKPAKNTGIVSSFFTYTGPSH---GTQWDEIDIEFLGKDT 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lichenase and Coding Sequences
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                                                                                                                                                                                                          23; Mismatches
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                                                                                                                                                                                                                                  Score 225; DB 3; Pred. No. 3.3e-15;
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Pred. No. 1.2e-15;
5; Mismatches 76;
                                                                                                                                                                                                                                                   Length 238;
                                                                                                                                                                                                            Indels 16; Gaps
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US-09-286-690-11
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NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08103998 Patent No. 5470725
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Best Local S
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APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Lichenase and Coding Sequences FILE REFERENCE: 55-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Clostridium thermocellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 242
                                                    ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                              STREET: 1800 Dia
CITY: Alexandria
STATE: VA
CLASSIFICATION:
                  APPLICATION NUMBER: US/08/103,998 FILING DATE:
                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 REYGGSYPYKSGEYRTKSFFGYGYYEVRMKAAKNVGIVSSFFTYTGPS---DNNPWDEID 136
                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQE 118
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                                                                                                                                                                                                                                                  1800 Diagonal Road, P.O.
                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                         Von Wettstein, Dietrich
VENTION: A Thermostable (1,3-1,4)-beta-Glucanase
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                                                                                                                                                                                                                                                                                                                                                                                      Hofemeister, Jurgen
Thomsen, Karl Kristian
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35.6%;
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Pred. No. 6.2e-15;
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CURRENT APPLICATION NUMBER: US/09/286,690
CURRENT FILLING DATE: 1999-04-05
EARLIER APPLICATION NUMBER: US 60/027,882
EARLIER FILLING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: PCT/US97/17811
EARLIER FILLING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 2
LENGTH: 245
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                                                                                                                                                                                                                                                                                                  ; TYPE: PRT ; ORGANISM: Orpinomyces sp. PC-2 US-09-286-690-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Li, Xin-Liang
APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Hulzhong
TITLE OF INVENTION: Lichenase and Coding Sequences
FILE REFERENCE: 55-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09286690
Patent No. 6103511
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Best Local Similarity
                                                                                                                                                                                                                                                         Query Match
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NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3030
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 836-9300
TELEFAX: (703) 836-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 895149
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
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119 VRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWV 166
                                             137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 IPAAPGK--IMMNLWNGTGVDDWLGSYNGVN-PIYAHYDWMRYRK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 VSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 TKVQFNYYTNGAG---NHEKFADLGFDAANAYHTYAFDWQPNSIKWYVDGQ-LKHTATTQ 194
                                                                                                                                                                                                           Local Similarity 32.9%; Pred. No. 1.7e-11; les 56; Conservative 16. Michael 17. Length 245;
                                                                                     59
                                                                                                                            83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGP---AHGTQWDEIDIEFLGKDT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                      5 KDFSGAELYTLEEVQ-----YGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                           IEFLGYDTTKVQFNYYTNGQGHH----EHIHYLGFDASQGFHTYGFFWARNSITWYVDGTA 193
                                                                                                                            RDGSG---YTCGEYRTKNYYGYGMFQVNMKPIKNPGVVSSFFTYTGPS---DGTKWDEID 136
                                                                                   IEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56;
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16-OCT-1991
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33.9%;
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Pred. No. 9.6e-15;
3; Mismatches 75
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RESULT 11
US-09-159-106-2
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US-08-824-707-2
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.7%; Score 154.5; DB 3
Best Local Similarity 28.5%; Pred. No. 8.1e-08;
Matches 53; Conservative 28; Mismatches 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-878-9655 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                           284 DATTPF
                                                                                                                 177 EGGSDF 182
                                                                                                                                                                                                                                                                                                           131 YTSARLTTQGNVQPQFGRIEARIQIPRGQGIWSAFWMV--GANLPD-TPWPTSGEIDIME 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 VYTA----YDNIPDTPGKIMMNAWNGIGVDDWLRPFN-GRTNISAYYDWV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 212-00.
TELEPHONE: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 14-Apr CLASSIFICATION: 435
                                                                                                                                                                                                                                                                     61 VLGKNP----GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
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                                                                                                                                                                                         QEVRKTEGGQVSNLTGTQGLRFNLWSSESAAWVGQFDESKLPLFQFINWVKVYKYTPGQG 176
                                                                                                                                                                                                                               NVGNAPHEVHGTVHGPGYSGDNGIMGTYQHPQGWSFADD--FHTFGIDWTPGEITWLVDG
                                                                                                                                                       QEYHRVTTADVG----
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Halkier, Toxal
                                                                           289
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Diers, Ivan
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Savva, Demitris
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                                                                                                                                                   -ANQWV--FDQ---PFFLILN-VAIGGQWPGNP
                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                   37;
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                                                                                                                                                                                                                               245
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Sequence 2, Application US/09159106 Patent No. 6284509

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TITLE OF INVENTION: An Enzyme With -1,3-Glucanase TITLE OF INVENTION: Activity
FILE REFERENCE: 4693.204-US
CURRENT APPLICATION NUMBER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER FILING DATE: 1996-12-04
EARLIER APPLICATION NUMBER: 0427/96
EARLIER APPLICATION NUMBER: 0085/96
EARLIER APPLICATION NUMBER: 0085/96
EARLIER APPLICATION NUMBER: 007/00160
EARLIER APPLICATION NUMBER: 007/00160
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; SEQ ID NO 2

; LENGTH: 263

; TYPE: PRT

; ORGANISM: Oerskovia xanthineolytica

US-09-159-106-2
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US-09-159-106-11
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                                                             NUMBER OF SEQ ID NOS: 15
SOFTWARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 11
LENGTH: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/09159106 Patent No. 6284509
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Best Local Similarity
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EARLIER FILING DATE: 1996-12-04
EARLIER APPLICATION NUMBER: 0885/96
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1997-04-14
NUMBER OF SEQ ID NOS: 15
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APPLICANT: Diers, Ivan
APPLICANT: Halkier, Torben
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Halkier, Torben APPLICANT: Hedegaard, Lisbeth
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ferrer, Pau
APPLICANT: Diers, Ivan
APPLICANT: Halkier, Torben
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Halkier, Torben APPLICANT: Hedegaard, Lisbeth
                 ORGANISM: Oerskovia xanthineolytica
                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGPGYSGGSGITGMYQHPQGWSFADTFHTFAVDWKPGEITWFVDGQQFHRVTRASVG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QYGRIEARIQIPRGQG-IWPAFWMLGGS--FPGTPWPSGEIDIM-ENVG-FEPHRVHGTV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---ANAWV--FDQ---PFFLILN-VAVGGQWPGYPDGTTQLPQQMKVDYV 234
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25.9%;
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                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Oerskovia xanthineolytica US-09-159-106-13
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 1
SOFTWARE: FASTSEQ for V
SEQ ID NO 13
LENGTH: 303
LTYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: An Enzyme With -1,3-Glu TITLE OF INVENTION: Activity FILE REFERENCE: 4693.204-US CURRENT APPLICATION NUMBER: US/09/159,106 CURRENT FILING DATE: 1998-09-23 EARLIER APPLICATION NUMBER: 0427/96 EARLIER APPLICATION NUMBER: 0885/96 EARLIER FILING DATE: 1996-18-96 EARLIER FILING DATE: 1996-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/09159106 Patent No. 6284509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ferrer, Pau APPLICANT: Diers, Ivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: PCT/DK97/00160 EARLIER FILING DATE: 1997-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Halkier, Torben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hedegaard, Lisbeth
 287
                                                                                                      131
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                                187 TDNFDTFDGS
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                                                                                                                                                                         71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 QYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWV---EVDI-EVLGKNP----GSFQ 70
                                                                                                                                                                                                                                             19 QYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWV---EVDI-EVLGKNP----GSFQ 70
                                                                                                                                                                                                                                                                               Local Similarity
les 52; Conserv
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VRVYDNGSGS
                                                                                                                                                                       SNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNL 130
                                                                                                                                                                                                          QYGRIEARIQIPRGQG-IWPAFWMLGGS--FPGTPWPSSGEIDIMENVGFEPHRVHGTVH 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNPGTGLPTGTGAVRAANGMCVDVPWADPTDGNPVQIVTCSGNAAQTWTRGS---DGT-V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QYGRIEARIQIPRGQG-IWPAFWMLGGS--FPGTPWPSSGEIDIMENVGFEPHRVHGTVH 190
                                                                                                                                       GPGYSGGSGI--TGMYQHPQGWSFADTFHTFAVDWKPGEITWFVDGQQFHRVTRASVG-- 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----ANAWVFDQPFFLILNVAVGGQWPGYPDGTTQLPQQMKVDYVRVYDNGSGSSSP 299
                                                                                                    TGTQGLRENLWSSESAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGS----DFTLDW 186
                                                                                                                                                                                                                                                                               Conservative
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                                  196
                                                                                                                                                                                                                                                                                                                                                                                                                                           for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222
                                                                   -ANAWV--FDQ---PFFLILN-VAVGGQWPGYPDGTTQLPQQMKVDY
                                                                                                                                                                                                                                                                                                9.8%;
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                                                                                                                                                                                                                                                                            Score 140.5; DB 4;
Pred. No. 2.2e-06;
""" tches 74;
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Pred. No. 2.1e-06;
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RESULT 15
US-08-712-072C-3
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US-08-712-072C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BOGOSLAN, Elizabeth A.
RRGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 63475/97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0844 or 286-0082
TELES: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPER: ARIAC
                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 9.3%; Score 133.5; DB 2; Best Local Similarity 23.7%; Pred. No. 9.9e-06; Matches 44; Conservative 34; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Applic Patent No. 5925541
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NOTA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: ORIGINAL SOURCE:
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: ENDO-BETA-GALACTOSIDASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                    209
                                                                                                                                                                                                          115
                                                                                        269 VRVYRW 274
                                                                                                                            166 VKVYKY 171
                                                                                                                                                                                                                                              152 MEHVGFNPDVVHGTVHTKAYNHLLGTQRGGSIR---VPTARTDFHVYAIEWTPEEIRWFV 208
                                                                                                                                                                                                                                                                                    60
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STATE: NY
                                                                                                                                                                                                                                                                                                                       93 REYTSARLVTRGKASWTYGRFEIRARLPSGRGTWPAIWMLPDRQTYGSAY-WPDNGEIDI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                             5 KDFSGAELYTLEEVQ--YGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWV---EVDI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                      DGQEVRKTEGGQVSNLTG-----TQGLRFNLWSSESAAWVGQ--FDESKLPLFQFINW 165
                                                                                                                                                                  DDSLYYRFPNERLTDPEADWRHWPFDQPFHLIMNIAVGGAWGGQQGVDPEAFPAQLVVDY 268
                                                                                                                                                                                                                                                                                -EVLGKNP----GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTV 114
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                                                                                                                                                                                                                                                                                                                                                                                                   85; Indels
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Search completed: January
Job time : 11.5069 secs
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US-08-712-072C-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MS-DOS SOFTWARE: ASCII CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/712,072C FILING DATE: 11-SEP-1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: CILLOR CREEK PRIOR APPLICATION NUMBER: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0824 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, Elizabeth A
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 63
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: PHYPOTHETICAL: NO ANTI-SENSE: NO
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CORRESPONDENCE ADDRESS:
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                                                                           306
                                                                                                                                                                                           121 KTEGGQVSNLTGTQGLRFNLWSSESA---
                                                                                                                                                                                                                                                                                                         157 LPLFQFINWVKVYKY 171
                                                                                                                                                       260 KVTNQQ--------WYSTAAPNNPNAPFDEPFYLIMNLAVGGNFDGGRTPNASD 305
                                                                                                                                                                                                                                   200 RLPGSVSGTIHFGGQWPVNQSSGGDYHFPEGQTFANDYHVYSVVWEEDNIKWYVDGKFFY 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                   64 KNPGSFQSNIITG---KAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                           IPATMQVDYVRVYKF
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20.5%;
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Result
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Maximum DB
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Qy 2 VSAKDFSGAELYTLEEVQYGKFEARNKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEV 61	:g148575; PIDN: polysaccharide pore 1340; DB 2 ed. No. 1.5e-10 Mismatches	RESULT 1 A44507 A44507 A44507 Iicheninase (EC 3.2.1.73) - Fibrobacter succinogenes C; Species: Fibrobacter succinogenes C; Species: Fibrobacter succinogenes C; Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 08-Oct-1999 C; Accession: A44507 R; Teather, R.M.; Erfle, J.D. J. Bacteriol. 172, 3837-3841, 1990 J. Bacteriol. 172, 3837-3841, 1990 A; Title: DNA sequence of a Fibrobacter succinogenes mixed-linkage beta-glucanase (1 A; Reference number: A44507; MUID:90299807; PMID:2193918	30 142 9.9 472 2 S48564 probable membrane 31 141.5 9.8 289 2 T06166 xyloglucan endo-1, 33 140.5 9.8 310 2 A86239 xyloglucan endo-1, 34 140 9.7 305 2 G88568 protein T10024.17 35 139.5 9.7 286 2 T06202 protein T20024.17 36 133.5 9.3 286 2 T06202 xyloglucan endo-1, 37 132 9.2 295 2 T10210 xyloglucan endo-1, 38 131.5 9.1 292 2 T06201 xyloglucan endo-1, 39 129.5 9.0 1,324 2 T18265 endo-1,3(4)-beta-9 40 128 8.9 283 2 T07678 xyloglucan endo-1, 41 127.5 8.9 269 2 T04514 42 127 8.8 292 2 T04514 xyloglucan endo-1, 43 125.5 8.7 277 2 JE0156 xyloglucan endo-1, 44 125 8.7 301 2 C87296 xyloglucan endo-1, 45 124 8.6 299 2 D84519 probable endoxylog	
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endo-beta-1,3-1,4 glucanase (licheninase).bglS [imported] - Bacillus halodurans (stp. Species: Bacillus halodurans C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001 C;Accession: H84053 R;Takaki, V.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132

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RESULT 3
A48378
ALCHeninase (EC 3.2.1.73) - Bacillus brevis
N.Alternate names: lichenase
N.Alternate names: lichenase
C:Specles: Bacillus brevis
C:Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 07-May-1999
C.Accession: A48378
C.Accession: A48378
R:Louw, M.E.; Reid, S.J.; Watson, T.G.
Appl. Microbiol. Blotechnol. 36, 507-513, 1993
A.Title: Characterization, cloning and sequencing of a thermostable endo-(1.3-1.4) beta-A; Reference number: A48378; MUID:93159752; PMID:7763386
A; Status: preliminary
A; Molecule type: nucleic acid
A; Residues: 1-252 <LOUV
A; Note: sequence extracted from NCBI backbone (NCBIN:124672, NCBIP:124673)
C:Superfamily: licheninase
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB06951.1; GSPDB:GNO:Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                          ----TENIPQTPQKIMMNLWPGVGVDGWTGVFDGDNTPVYSYYDWV----RYTP
                                                                                                                                                                                                                    GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                                                                                                                                           SARNYKAGELRTNDFYHYGLFEVSMKPAKVEGTVSSFFTY-TGEWDWDGDPWDEIDIEFL 148
                                                                                                                                                                                                                                                                                                SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WYDSQITFSNGIMRFAIDKE-----DDEEA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLG
                                                                                                                                               EGGQVSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP 173
                                                                                                                                                                                          GKDTTRIQFNYFTNGVGG----NEFYYDLGFDASESFNTYAFEWREDSITWYVNGEAVHTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- DKNIYSRDGMLILALTRKGQESFNGQVPRDDEPA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGDDNEEEPVEEVEEEPAEDEEVSVRPIGSAIYETFNTFNEDIWSIAHGWT-NGQMFNAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGSDFTLDWT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---TENIPQTPQKIMMNLWPGVGVDEWTGVFDGDNTPLHADYEWV----RYTPLEALDEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGQVSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP----GQGE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDTTRIQFNYFTNGVGG----NEFYYDLGFDASESFNTYAFEWREDSITWYVNGEAVHTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPYKAGELRTNDFYQYGLFEVSMKPAKVEGTVSSFFTY-TGEWDWDGDPWDEIDIEFLG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82;
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                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.5%;
                                                                                                                                                                                                                                                                                                                                                                                 18.5%; Score 265.5; DB 2; 35.8%; Pred. No. 7.9e-15;
                                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 266.5; DB 2; Pred. No. 3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                               Mismatches
  sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----DNFDTFDGSRWG-KGDWTFDGNRVDLT 213
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Length
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licheninase (EC 3.2.1.73) precursor - Bacillus subtilis N;Alternate names: 1,3-1,4-beta-D-glucan 4-gluconohydrolase; bet N;Contains: licheninase E-1; licheninase E-2 C;Species: Bacillus subtilis C;Date: 30-Jun-1988 #sequence_revision 13-Mar-1998 #text_change C;Accession: I40370; B69594; A22914; A90026; A90027; JU0110 R;Wolf, M.; Geczi, A.; Simon, O.; Borriss, R. Microbiology 141, 281-290, 1995 A;Title: Genes encoding xylan and beta-glucan hydrolysing enzymes A;Reference number: I40370; MUID:95219081; PMID:7704256 A;Accession: I40370
                                                                                                                             A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Species: Bacillus sp.
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change C:Accession: I40453; S32688
R:Tabernero, C.; Coll, P.M.; Fernandez-Abalos, J.M.; Perez, P.; Appl. Environ. Microbiol. 60, 1213-1220, 1994
A;Title: Cloning and DNA sequencing of BanA a gene encoding an A;Reference number: 140453; MUID:94288605; PMID:7517127
A;Accession: I40453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:246862; NID:g599673; PIDN:CAA86922.1; PID:g599674
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Be.
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
C.; Bron, S.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-242 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
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A;Molecule type: DNA
A;Residues: 1-276 <RES>
A; Molecule type: DNA
A; Residues: 1-242 <KUN>
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C;Keywords: glycosidase; hy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z12151; NID:g296931; PIDN:CAA78135.1; C;Genetics:
                                                                  A; Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                        A; Accession: B69594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TENIPQTPQKIMMNLWPGIGVDGWTGRFNGEDTPVVTQYDWV---KYTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKIQFNYFTNGVGG---NEHYHELGFDAADDFNTYAFEWRPESIRWFVNGELVHTA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKAGELRTNDFYHYGLFEVSMKPAKSTGTVSSFFTY-TGPWDWENDPWDEIDIEFLGKDT
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36.1%;
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Pred. No. 2.8e-13;
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A;Cross-references: GB:Z99124;

source:

168

GB:AL009126; NID:g2636442;

PIDN:CAB15943.1; PID:g26364

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A; Mulecule: 1-802 < FFLI>
A; Residues: 1-802 < FFLI>
A; Cross-references: GB: S61204; NID: g385910; PIDN: AAB26620.1; PID: g385911
A; Cross-references: GB: S61204; NID: g385910; PIDN: AAB26620.1; PID: g385911
A; Note: sequence extracted from NCBI backbone (NCBIN: 131871, NCBIP: 131872)
C; Superfamily: endo-1, 4-beta-xylanase homology: Thermotoga xylanase A amino-terminal
F; 42-239/Domain: endo-1, 4-beta-xylanase homology: <XYL>
F: 259-401/Domain: Thermotoga xylanase A amino-terminal repeat homology <TXA>
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
A36910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide F:1-28/Domain: signal sequence #status predicted <SIG> F:29-242/Product: licheninase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-23'S',25-82,'S',84-242 <TEZ>
A;Cross-references: DBJ:D00518; NID:g216243;
A;Cross-references: DBJ:D00518; NID:g216243;
A;Experimental source: strain Y-25, clone pLE1
R;Yuuki, T.; Tezuka, H.; Yabbuchi, S.
Agric. Biol. Chem. 53, 2341-2346, 1989
A;Title: Purification and some properties of t
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                                                                                                                                                                                                                       A; Reference number: A36910; A; Accession: A36910
                                                                                                                                                                                                                                          A; Title: A bifunctional enzyme, with separate xylanase and A; Reference number: A36910; MUID:93259938; PMID:8491715
                                                                                                                                                                                                                                                                                         R; Flint, H.J.; Mar
J. Bacteriol. 175,
                                                                                                                                                                                                                                                                                                                                     xylanase, beta(1,3-1,4)-glucanase - Ruminococcus flavefaciens
C;Species: Ruminococcus flavefaciens
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change
C;Accession: A36910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: source was hyperproducing strain HL-25 A;Note: the amino ends of the mature forms of H
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A;Title: Construction of a beta-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-203, 'L', 205-242 < MUR>
A; Cross-references: EMBL: X00754; NID: 939818;
A; Experimental source: strain C120
                                                                                                                                                                                              A; Status: preliminary
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Best Local :
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                                                                                                                                                                                                                                                                                                               Martin, J.; McPherson, C.A.; Daniel, A.S.;
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A; Rocession: A29091
A; Molecule type: DNA
A; Residues: 1-239 <HOF>
A; Cross-references: GB:M15674; NID:g143009;
A;Molecule type: DNA
A;Residues: 1-334 <SCH>
A;Cross-references: EMBL:X63355; NID:g40697; PIDN:CAA44959.1; PID:g40698
C;Genetics:
                                                                                                                                                                                                 licheninase (EC 3.2.1.73) licB precursor - Clostridium thermocellum %Alternate names: beta-1,3-1,4-glucanase licB; lichenase licB C;Species: Clostridium thermocellum C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-C;Accession: S23498; S22137
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A; Gene: bglA
C; Superfamily: licheninase
C; Keywords: glycosidase; hydro
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A;Title: The beta-glucanase gene from Bacillus amylo A;Reference number: A91564; MUID:87192007; PMID:3106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: 1,3-1,4-beta-D-glucan 4-glucanohydrolase; C;Species: Bacillus amy!cliquefaciens C;Date: 10-Sep-1999 #secuence_revision 10-Sep-1999 #text_charclession: A29091 R;Hofemeister, J.; Kurtz, A.; Borriss, R.; Knowles, J. R;Hofemeister, J.; Kurtz, A.; Borriss, R.; Knowles, J.
                                                                                                                                        R;Schimming, S.; Schwarz, W.H.; Staudenbauer, Eur. J. Biochem. 204, 13-19, 1992
A;Title: Structure of the Clostridium thermoo
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                                                                                                     A; Reference number:
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                                                                                  S23498
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                                                                                                                                        Clostridium thermocellum gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.6%; Score 238.5; DB 1 34.3%; Pred. No. 1.3e-12; tive 26; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene from Bacillus amyloliquefaciens
MUID:87192007; PMID:3106158
                                                                                                     MUID:92155194;
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                                                                                                  PMID:1740123
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                                                                                                                                                                                W.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: endo-beta-1,3-1,4-D-glucanase; C;Species: Bacillus licheniformis C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Accession: S15388
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C; Species: Bacillus
                          licheninase (EC 3.2.1.73) precursor [validated] - Bacillu N;Alternate names: endo-beta-1,3-1,4-glucanase; lichenase
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Eur. J. Biochem. 197, 337-343, 1991
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$15388
Licheninase (EC 3.2.1.73) - Bacillus licheniformis
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A; Residues: 1-243 <LLO>
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                                                                                                                                                                                                                                                                                     EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
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                                                                                                                                                                                                                          ATTQIPQTPGK--IMMNLWNGAGVDEWLGSYN-GVTPLSRSLHWVRYTK 242
                                                                                                                                                                                                                                                                                                                                                    GKDTTKVQFNYYTNGVG----NHEKIVNLGFDAANSYHTYAFDWQPNSIKWYVDGQ-LKHT
                                                                                                                                                                                                                                                                                                                                                                                                                   GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAKDFSGAELYTLEEVOYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62
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30.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 229.5; DB 1
Pred. No. 7.8e-12;
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Pred. No. 2.7e-12;
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A; Description: catalyzes the hydrolysis of 1,4-beta-D-glucosid. (Superfamily: licheninase C; Keywords: glycosidase; hydrolase; polysaccharide degradation F;1-26/Domain: signal sequence #status predicted <PRO>F;27-237/Product: licheninase #status predicted <MAT>F;56-85/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 173, 7705-7710, 1991
A;Title: Two beta-glycanase genes are clustered in Bacillus polymyxa: molecular cloni
A;Reference number: S19011; MUID:92041687; PMID:1938968
A;Accession: S19012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                licheninase (EC 3.2.1.73) precursor - Bacillus polymyxa N;Alternate names: endo-beta-1,3-1,4-glucanase; lichenase C;Species: Bacillus polymyxa C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_C;Accession: S19012 R;Gosalbes, M.J.; Perez-Gonzalez, J.A.; Gonzalez, R.; Nav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Description: catalyzes the hydrolysis of 1,4-beta-D-glucosid C;Superfamily: licheninase C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;1-25/Domain: signal sequence #status predicted F;1-25/Domain: signal sequence
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A;Contents: annotation; X-ray crystallography, 2.3 angstroms, residues 26-37,'p',39-2
A;Note: recombinant form with residues 26-41 from Bacillus amyloliquefaciens expresse
R;Keitel, T.; Simon, O.; Borriss, R.; Heinemann, U.
Proc. Natl. Acad. Sci. U.S.A. 90, 5287-5291, 1993
A;Title: Molecular and active-site structure of a Bacillus 1,3-1,4-beta-glucanase.
A;Reference number: A47562; MUID:93281743; PMID:8099449
A;Contents: annotation; X-ray crystallography, 2.3 angstroms
A;Contents: annotation; X-ray crystallography, 2.3 angstroms
A;Note: recombinant form with residues 26-41 from Bacillus amyloliquefaciens expresse
C;Function:
                                                                                                                                                                                                                             C; Function
                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-238 <GOS>
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A; Title: Structure of the beta-1,3-1,4-glucanase gene of A; Reference number: S11927; MUID:91109712; PMID:2274030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 C;Accession: S11927 C;R; Buettner, K.; Maentsaelae, P.
                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X57094; NID:g48815; PIDN:CAA40379.1;
                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the Brookhaven Protein Data Bank,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Hahn, M.; Heinemann, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-237 <BOR>
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A; Status: preliminary
   F;129/Active site:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 172
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   Glu #status
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predicted
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Pred. No. 1.5e-11;
3; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.A.; Gonzalez, R.; Navarro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-Nov-1995 #text_change 18-Jun-1999
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endo-1,3(4)-beta-glucanase family 16 [imported] - Clostridium
c;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_chang
C;Accession: D97245
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.;
                                                                                                  RESULT
D97245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: licheninase
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-27/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross references: EMBL:X58392
R;Zverlov, V.V.; Velikodvorskaya, G.A.
Biotechnol. Lett. 12, 811-816, 1990
A;Title: Cloning the Clostridium thermocellum thermostable laminarinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: JS0611; S18726
R;Zverlov, V.V.; Laptev, D.A.; Tishkov, V.I.; Velikodvorskaja, G.A.
Biochem. Biophys. Res. Commun. 181, 507-512, 1991
A;Title: Nucleotide sequence of the Clostridium thermocellum laminarinase A;Reference number: JS0611; MUID:92095946; PMID:1755832
A;Accession: JS0611
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A; Residues: 1-242 < ZVE2>
A; Cross-references: EMBL: X58392
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A; Accession: S18726
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A; Residues: 1-242 < ZVE1>
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Matches
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                                                                                                                                                                               VYR----GTRNIPVTPGKIMMNLWPGIGVDEWLGRYD-GRTPL
                                                                                                                                                                                                                    VRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPL 159
                                                                                                                                                                                                                                                                                                                                                                                 KDFSGAELYTLEEVQ-----YGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTNIPSTPGKIMMNLWNGTGVDSWLGSYNGAN-PLYAEYDWV---KYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKVQFNYYTNGVGGH----EKIINLGFDASTSFHTYAFDWQPGYIKWYVDG-VLKHT---A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FDCGEYRSTNNYGYGLYEVSMKPAKNTGIVSSFFTYTGPSH---GTQWDEIDIEFLGKDT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                                                                                                                                                                                                                                              IEFLGKDTTKVQFNWYKNGVGG----NEYLHNLGFDASQDFHTYGFEWRPDYIDFYVDGKK
                                                                                                                                                                                                                                                                                                   IEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQE 118
                                                                                                                                                                                                                                                                                                                                             REYGGSYPYKSGEYRTKSFFGYGYYEVRMKAAKNVGIVSSFFTYTGPS---DNNPWDEID 136
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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35.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 222.5; DB Pred. No. 3e-11;
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Pred. No. 1.8e-11;
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Zeng, Q.; Gibson,
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A;Cross-references: GB:AE008689; PIDN:AAL44856.1; PID:917742502; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; Karp, P.; Romero, P.; Ehang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jaly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: D97245
A;Status: preliminary
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C; Superfamily: licheninase
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A; Residues: 1-246 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: The Genome of the Natural Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ster,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kan
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                                                                                                                                                                 KDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGK 64
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--EVTDETKIPQNAQKIFFSLWGTDTLKDWMGKF
                                 GGQVSNLT----GTQGLRFNLWSSESAA-WVGQF
                                                                       NTGKVQLNQYIAAKGG----NEKLVPVEGGADAGFNDYAFVWEPQRLRYYVNGKLVH---
                                                                                                                                            RNFACGEIQTKGRYRYGTYEARMKAATGSGLNSAFFTYIGPT---DKKPHDEIDFEVLGK 145
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                                                                                                        NPGSFQSN-IITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTE 123
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M.; McCl
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C;Genetics:
A;Gene: AGR_L_1600
A;Map position: linear chromosome
C;Superfamily: licheninase
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A;Title: Genome Sequence of the Plant Pathogen and Blotechnology Agent Agrobacterium tum A;Reference number: A97359; PMID:11743194
A;Accession: C98231
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-289 <KUR>
A;Cross*references: GB;AE007870; PIDN:AAK89373.1; PID:g15159224; GSPDB:GN00170
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   1 MVSAKDFSGAELYTLEEVQY.....TRKGQESFNGQVPRDDEPAP 248
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(without alignments)
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xyloglucan endo-1,
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ДУ	Дb	Qy Db	Qy Db	Qy Db	Ques Best Mato	J. Bac A;Tilt. A;Tilt. A;Ref A;Acc A;Stai A;Molil A;Mos A;Cros C;Rey	RESULT A44507 Lichen C;Spec C;Date C;Acce		
242 RDDEPAP 248	82 FTLDWTDN	122 TEGGQVSNLTGTQ5LRFNLWSSESAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGSD 181 	62 LGKNPGSFQSNIITSKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRK 121 	2 VSAKDESGAELYTLEEVOYGKFEARMKMAAASGTVSSMELVONGSEIADGRPWVEVDIEV 61 	Query Match 99.6%; Score 1328; DB 2; Length 349; Best Local Similarity 100.0%; Pred. No. 1.5e-104; Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Te, J.D.  1037:3841, 1990  1037:3841, 1990  1037:3841, 1990  1037:3841, 1990  1044507; MUID:90299807; PMID:2193918  1044507; MUID:90299807; PMID:2193918  1059  10	RESULT 1 A44507 Aid+507 Licheninase (EC 3.2.1.73) - Fibrobacter succinogenes C;Species: Fibrobacter succinogenes C;Species: Maar-1993 #sequence_revision 03-Mar-1993 #text_change 08-Oct-1999 C;Accession: A44507	ALIGNMENTS	30 141.5 10.6 289 2 T06166 xyloglucan endotra 31 140.5 10.5 280 2 T02090 xyloglucan endo-1, 32 140.5 10.5 310 2 A86239 probable xyloglucan 33 140 10.5 305 2 G84568 probable membrane 34 139.5 10.5 286 2 T06202 probable membrane 35 138 10.4 422 2 S48264 probable membrane 36 133.5 10.0 286 2 S48201 licheninase (EC 3. 37 132 9.9 295 2 T10210 xyloglucan endo-1, 38 131.5 9.9 295 2 T10220 xyloglucan endo-1, 39 129.5 9.7 1324 2 T18265 endo-1, 349.9 teach of the contract of the cont
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endo-beta-1,3-1,4 glucanase (licheninase) bglS [imported] - Bacillus halodurans (strops to be sequence of the alkaliphilic bacterium Bacillus halodurans A; Reference number: A83650; MUID:20512582; PMID:11058132

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RESULT 2 H84053

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A; Experimental s
C; Genetics:
A; Gene: bglS
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A;Status: preliminary
A;
                                       RESULT
I40453
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N;Alternate names: lichenase
C;Species: Bacillus brevis
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 07-May-1999
C;Accession: A48378
R;Louw, M.E.; Reid, S.J.; Watson, T.G.
Appl. Microbiol. Biotechnol. 38, 507-513, 1993
A;Title: Characterization, cloning and sequencing of a thermostable endo-(1,3-1,4) beta-A;Reference number: A48378; MUID:93159752; PMID:7763386
A;Accession: A48378
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A48378
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A; Residues: 1-252 <LOU>
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licheninase (EC 3.2.1.73) -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SARNYKAGELRTNDFYHYGLFEVSMKPAKVEGTVSSFFTY-TGEWDWDGDPWDEIDIEFL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- DKNIYSRDGMLILALTRKGQESFNGQVPRDDEPA 247
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                                                                                                                                                                                             ----TENIPQTPQKIMMNLWPGVGVDGWTGVFDGDNTPVYSYYDWV---RYTP
                                                                                                                                                                                                                                                                   EGGOVSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP 173
                                                                                                                                                                                                                                                                                                                                                  GKDTTRTQFNYFTNGVGG----NEFYYDLGFDASESFNTYAFEWREDSITWYVNGEAVHTA
                                                                                                                                                                                                                                                                                                                                                                                                                     GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.9%; Score 265.5; DB 2; 35.8%; Pred. No. 4.8e-15; ative 24; Mismatches 74;
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A;Cross-references: EMBL:246862; NID:g599673; PIDN:CAA86922.1; PID:g599674
A;Cross-references: EMBL:246862; NID:g599673; A;Choss-references: EMBL:246862; NID:g599673; A;Choss-references: EMBL:246862; NID:g599673; A;Choss-references: EMBL:CAGNES-References: EMBL:CAGNES-References: Carter, N.M.;
C: Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galicci, A; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawar, K.; Ogdwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstta, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Reference number: A05580; MUID:93044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         licheninase (EC 3.2.1.73) precursor - Bacillus subtilis
N;Alternate names: 1,3-1,4-beta-D-glucan 4-gluconohydrolase; bet
N;Contains: licheninase E-1; licheninase E-2
C:Species: Bacillus subtilis
C;Date: 30-Jun-1988 #sequence_revision 13-Mar-1998 #text_change
C;Date: 30-Jun-1988 #sequence_revision 13-Mar-1998 #text_change
C;Accession: I40370; B69594; A29026; A90027; JU0110
R;Wolf, M; Geczi, A; Simon, O; Borriss, R.
Microbiology 141, 281-290, 1995
Microbiology 141, 281-290, 1995
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C;Jate: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 22-Jun-1999
C;Jate: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 22-Jun-1999
C;Accession: 140453; S32688
R;Tabernero, C; Coll, P.M.; Fernandez-Abalos, J.M.; Perez, P.; Santamaria, Appl. Environ. Microbiol. 60, 1213-1220, 1994
A;Title: Cloning and DNA sequencing to ByaA, a gene encoding an endo-beta-1
A;Reference number: 140453; MUID:94288605; PMID:7517127
A;Accession: 140453
A; Molecule type: DNA
A; Residues: 1-242 <KUN>
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A;Molecule type: DNA
A;Residues: 1-242 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microbiology 141, 281-290, 1995
A;Title: Genes encoding xylan and beta-glucan hydrolysing
A;Reference number: I40370; MUID:95219081; PMID:7704256
A;Accession: I40370
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C; Superfamily: licheninase
C; Keywords: glycosidase; hy
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                                                                     A; Status: preliminary; nucleic acid
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Pred. No. 1.8e-13;
                                                                             sequence not shown; translation
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A;Cross-references: GB:Z99124; A;Experimental source: strain 1

: GB:AL009126; NID:g2636442; PIDN:CAB15943.1; PID:g26364 168

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A; Residues: 1-802 <FLI>A; Residues: 1-802 <FLI>A; Cross references: GB:561204; NID:g385910; PIDN:AAB26620.1; PID:g385911
A; Cross references: GB:561204; NID:g385910; PIDN:AAB26620.1; PID:g385911
A; Note: sequence extracted from NCBI backbone (NCBIN:131871, NCBIP:131872)
C; Superfamily: endo-1.4-beta-xylanase homology; Thermotoga xylanase A amino-terminal
F; 42-239/Domain: endo-1.4-beta-xylanase homology <XYL>
F; 259-401/Domain: Thermotoga xylanase A amino-terminal repeat homology <TXA>
                                                                                                                                                                                                                                                                                                                                    xylanase, beta(1,3-1,4)-glucanase - Ruminococcus flavefaciens
C;Specias: Ruminococcus flavefaciens
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change
C;Accession: A36910
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A36910
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                                                                                                                                                                                                          A;Title: A bifunctional enzyme, with separate xylanase and A;Reference number: A36910; MUID:93259938; PMID:8491715 A;Accession: A36910
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C; Keywords: extracellular protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Purification and some properties of two enzymes f A;Reference number: A90027 A;Contents: annotation A;Note: source was hyperproducing strain HL-25 with gene f A;Note: the amino ends of the mature forms of E-1 and E-2 C;Genetics: A;Gene: bglS
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A;Residues: 1-23,'S',25-82,'S',84-242 <TEZ>
A;Cross-references: DDB::D00518; NID:g216243; PIDN:BAA00405.1;
A;Experimental source: strain Y-25, clone pLE100
                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-802 <FLI>
                                                                                                                                                                                                                                                                                R;Flint, H.J.; Martin, J.; McPherso J. Bacteriol. 175, 2943-2951, 1993
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Agric. Biol. Chem. 53, 2341-2346, 1989
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A; Residues: 1-203, 'L', 205-242 < MUR>
A; Cross-references: EMBL: X00754; NID: 939818;
A; Experimental source: strain C120
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Nucleic Acids Res. 12, 5355-5367, 1994
A;Title: The DNA sequence of the gene and genetic control sites
A;Reference number: A93526; MUID:84272222; PMID:6087283
A;Accession: A22914
A;Molecule type: DNA
A;Residues: 1-203,'L',205-242 <MUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
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                                                                                                                                                                                                                                                                                                             McPherson,
                                                                                                                                                                                                                                                                                                          C.A.;
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                                                                                                                                                                                                                                                                                                             Zhang, J
                                                                                                                                                                                                                                                           beta(1,3-1,4)-glucanase doma
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A:Experimental source: s
C:Genetics:
A:Gene: bglA
C:Superfamily: lichenina
C:Keywords: glycosidase;
                                                                                                                A;Title: Structure
l cellulace
                                                                                                                            R;Schimming, S.; Schwarz, W.H.; Staudenbauer, Eur. J. Biochem. 204, 13-19, 1992
A;Title: Structure of the Clostridium thermoc
                                                                                                                                                                                       C;Species: Clostridium thermocellum C;Date: 10-Sep-1999 #sequence_revision C;Accession: S23498; S22137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Hofemeister, J.; Kurtz, A.; Borriss, Gene 49, 177-187, 1986
A;Title: The beta glucanase gene from !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: 1,3-1,4-beta-D-gluca
C;Species: Bacillus amyloliquefaciens
C;Date: 10-Sep-1999 #sequence_revision
C;Accession: A29091
 A;Cross-references:
C;Genetics:
                                       A; Molecule type: DNA
A; Residues: 1-334 <SCH>
                                                                           A; Reference number: A; Accession: S23498
                                                                                                                                                                                                                                                licheninase (EC 3.2.1.73) licB precursor - Clostridium thermocellum N; Alternate \ names: \ beta-1,3-1,4-glucanase \ licB; \ lichenase \ licB
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A; Residues: 1-239 <HOF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A91564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A29091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             licheninase (EC 3.2.1.73) beta - Bacillus amyloliquefaciens N; Alternate names: 1,3-1,4-beta-D-glucan 4-glucanohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: licheninase; hydrolase; polysaccharide degradation; Keywords: glycosidase; hydrolase; polysaccharide degradation
Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKNPGSFQSNIITGXAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE----GTPWDEIDIEFL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YSGGEFRTNNFYHYGYYECSMQAMKNDGVVSSFFTYTGPS----DDNPWDEIDIEILGKNT
                                                                                                                                                                                                                                                                                                                                                                 ATTQIPAAPGK---IMMNLWNGTGVDDWLGSYNGVN-PIYAHYDWMRYRK
                                                                                                                                                                                                                                                                                                                                                                                                   EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                        GKDTTKVQFNYYTNGAG----NHEKFADLGFDAANAYHTYAFDWQPNSIKWYVDGQ-LKHT
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                     EMBL: X63355;
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                                                                                                                                  Clostridium thermocellum gene
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MUID:87192007; PMID:3106158
                                                                                              MUID:92155194;
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BE20/78
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                   NID: 940697; PIDN: CAA44959.1;
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Pred. No. 8.6e-13;
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Pred. No. 1.8
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                                                                                              PMID:1740123
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                                                                                                                                                                       W.L.
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                   PID:g40698
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N;Alternate names: endo-beta-1,3-1,4-D-glucanase; lichenase
C;Species: Bacillus licheniformis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S15388
R;Lloberas, J.; Perez-Pons, J.A.; Querol, E.
Eur. J. Blochem. 197, 337-343, 1991
A;Title: Molecular cloning, expression and nucleotide sequence of the endo-b.
A;Reference number: S15388; MUID:91224124; PMID:2026156
A;Ccession: S15388
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-243 <LLO>
A;Cross-references: EMBL:X57279; NID:g39558; PIDN:CAA40547.1; PID:g39559
C;Superfamily: licheninase
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                  RESULT
S11927
N; Alternate
C; Species: I
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S15388
                    licheninase (EC 3.2.1.73) precursor [validated] N;Alternate names: endo-beta-1,3-1,4-glucanase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVNRDG-RIDSTDLTMLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPTPTPTIAPSTPTNPNLPLKGDVNGDGHVNSSDYSLFKRYLLRVIDRFPVGDQS---VA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEFLGKDTTKVQFNWYKNGVGG---NEYLHNLGFDASQDFHTYGFEWRPDYIDFYVDGKK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDFSGAELYTLEEVQ-----YGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVD 58
                                                                                                                                                         ATTQIPQTPGK - - IMMNLWNGAGVDEWLGSYN - GVTPLSRSLHWVRYTK
                                                                                                                                                                                                EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                                                                                                                                                                                                                            GKDTTKVQFNYYTNGVG----NHEKIVNLGFDAANSYHTYAFDWQPNSIKWYVDGQ-LKHT
                                                                                                                                                                                                                                                                                     GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                                                                                                                                                                                                SYNKFDCGENRSVQTYGYGLYEVNMKPAKNVGIVSSFFTYTGPT---DGTPWDEIDIEFL 140
                                                                                                                                                                                                                                                                                                                                                                            SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DWTFDGNRVDLTDKNIYSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VYR----GTRNIPVTPGKIMMNLWPGIGVDEWLGRYD-GRTPLQAEYEYVKYYPNGVPQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQE 118
    Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.2.1.73) - Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          17.2%; Score 229.5; DB 33.7%; Pred. No. 5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                     25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.80
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 237; DB 1;
Pred. No. 1.8e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GQGE-GGSDFT-----LDWTDNFDTFDGSRWGKG
                      lichenase

    Bacillus macerans

                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                       76;
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                                                                                                                                                         242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243;
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A; Description: catalyzes the hydrolysis of 1,4-beta-D-glucosid C; Superfamily: licheninase C; Keywords: glycosidase; hydrolase; polysaccharide degradation F;1-26/Domain: signal sequence #status predicted <PRO>F;27-237/Product: licheninase #status predicted <MAT>
                                                                                                                                                                                                       A;Cross-references: EMBL:X57094; NID:g48815; PIDN:CAA40379.1; C;Function:
                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 173, 7705-7710, 1991
A;Title: Two beta-glycanase genes are clustered
A;Reference number: S19011; MUID:92041687; PMID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  licheninase (EC 3.2.1.73) precursor - Bacillus polymyxa N;Alternate names: endo-beta-1,3-1,4-glucanase; lichenase C;Species: Bacillus polymyxa C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_C;Accession: S19012 R;Gosalbes, M.J.; Perez-Gonzalez, J.A.; Gonzalez, R.; Nava
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
S19012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: A67074; PDB:LMAC
A;Contents: annotation; X-ray crystallography, 2.3 angstroms, residues 26-37,'p',39-2
A;Contents: annotation; X-ray crystallography, 2.3 angstroms, residues 26-37,'p',39-2
A;Note: recombinant form with residues 26-41 from Bacillus amyloliquefaciens expresse
R;Keitel, T.; Simon, O.; Borriss, R.; Heinemann, U.
Proc. Natl. Acad. Sci. U.S.A. 90, 5287-5291, 1993
A;Title: Molecular and active-site structure of a Bacillus 1,3-1,4-beta-glucanase.
A;Reference number: A47562; MUID:93281743; PMID:8099449
A;Contents: annotation; X-ray crystallography, 2.3 angstroms
A;Note: recombinant form with residues 26-41 from Bacillus amyloliquefaciens expresse
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Gen. Genet. 222, 278-283, 1990
A;Title: Structure of the beta-1,3-1,4-glucanase gene of A;Reference number: S11927; MUID:91109712; PMID:2274030 A;Accession: S11927
A;Status: preliminary
                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-238 <GOS>
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                              F;56-85/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: S19012
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A; Residues: 1-237 <BOR>
F;129/Active site:
                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;128/Active site: Glu #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Hahn, M.; Heinemann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: X55959; NID: g296715; PIDN: CAA39426.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55-84/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-237/Product:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGP---AHGTQWDEIDIEFLGKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                         catalyzes the hydrolysis of 1,4-beta-D-glucosidic
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      Glu #status
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   predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J.A.; Gonzalez, R.; Navarro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
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No. 9.7e-12;
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PMID:1938968
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endo-1,3(4)-beta-glucanase family 16 [imported] - Clostridium
C;Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_chang
C;Accession: D97245
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.;
                                                                                                       RESULT
D97245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: lam1
C;Superfamily: licheninase
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-242/Product: endo-1,3(4)-beta-glucanase #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X58392
R;Zverlov, V.V.; Velikodvorskaya, G.A.
Biotechnol. Lett. 12, 811-816, 1990
A;Title: Cloning the Clostridium thermocellum thermostable laminarinase
A;Reference number: S18726
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A:Molecule type: DNA
A:Residues: 1-242 < ZVE2>
A:Cross-references: EMBL:X58392
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C;Accession: JS0611; S18726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: laminarinase C;Species: Clostridium thermocellum
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A; Accession: S18726
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A; Residues: 1-242 <ZVE1>
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                                                                                                                                                                                                                        VRKTEGGOVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPL 159
                                                                                                                                                                                                                                                                                                                                                                                         KDFSGAELYTLEEVQ-----YGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVD 58
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                                                                                                                                                                                                                                                                  IEFLGKDTTKVQFNWYKNGVGG---NEYLHNLGFDASQDFHTYGFEWRPDYIDFYVDGKK 193
                                                                                                                                                                                                                                                                                     IEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQE 118
                                                                                                                                                                                                                                                                                                                                                 REYGGSYPYKSGEYRTKSFFGYGYYEVRMKAAKNVGIVSSFFTYTGPS---DNNPWDEID 136
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35.6%;
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34.5%;
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Pred. No. 2e-11;
2; Mismatches
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Pred. No. 1.2e-11;
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                                      14-Sep-2001 #text_change 30-Sep-2001
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Zeng, Q.; Gibson,
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A.Title: The Genome of the Natural Genetic A.Paference number: AB2577; PMID:11743193
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C;Accession: AB3055
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A;Molecule type: DNA
A;Residues: 1-246 <KUR>
A;Cross-references: GB:AE001437; P:
A;Experimental source: Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4833-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: D97245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
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                                                                                                                                                                                                                                                                                                                           A; Map position: linear chromosome C; Superfamily: licheninase
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A; Residues: 1-263 <KUR>
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C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---TSNIPTHPGKVMMNLWPGIGVDSWLGAYD-GVTPVKAYYNWA---MYNP 245
                                      GGQVSNLT----GTQGLRFNLWSSESAA-WVGQF
                                                                                                                  NPGSFQSN-IITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTE 123
                                                                                                                                                              RNFACGEIQTKGRYRYGTYEARMKAATGSGLNSAFFTYIGPT---DKKPHDEIDFEVLGK 145
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--EVTDETKIPQNAQKIFFSLWGTDTLKDWMGKF
                                                                                NTGKVQLNQYIAAKGG----NEKLVPVEGGADAGFNDYAFVWEPQRLRYYVNGKLVH---
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Pred. No. 5.4e-10;
6; Mismatches 56
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Pred. No. 2.7e-11;
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R;Goodner, B; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Llu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-238, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; PMID:11743194
A; Recession: C98231
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-289 <KUR>
A; Cross-references: GB:AE007870; PIDN:AAK89373.1; PID:g15159224; GSPDB:GN00170
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A;Map position: linear chromosome
C;Superfamily: licheninase
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                                                                                               В
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Best Local Similarity 35.1
Matches 54; Conservative
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                                                                                                                                     124 GGQVSNLT----GTQGLRFNLWSSESAA-WVGQF 152
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        DB
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US-08-103-998-2

US-09-286-690-10

US-09-286-690-1

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US-09-286-690-1

US-08-103-998-4

US-09-159-106-1

US-08-712-072C-3

US-08-712-072C-3

US-09-262-653A-4

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US-09-262-653A-4

US-09-262-731-8

US-09-330-945-3

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US-09-330-945-3

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	SULT 1 -09-286-690-12 Sequence 12, Applica Patent No. 6103511 GENERAL INFORMATION: APPLICANT: Li, Xin- APPLICANT: Chen, Hu TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: 55- CURRENT FILING DATE EARLIER APPLICATION EARLIER APPLICATION EARLIER FILING DATE ORGANIES PATON SEO ID NO 12 ORGANISM: FIDROBAC OP-286-690-12 Ouery Match Best Local Similarit Best Local Similarit Best Local Similarit	109.5 108.5 108.5 108.5 108.5 107.5 105.5 105.5 105.5 103.5 103.5 103.5 103.5 98.5
WYKYYK	990-12 12, Application US/ . 610351 III: NFORMATION: IT: Li, Xin-Liang IT: Chen, Huizhong IT: Chen, Lichena- FERENCE: 55-96 APPLICATION NUMBER: FILING DATE: 1999-0 APPLICATION NUMBER: FILING DATE: 1999-1 APPLICATION NUMBER: FILING DATE: 1997-1 PERIOR DATE: 1997-1 APPLICATION NUMBER: FILING DATE: 1997-1 APPLICATION NUMBER: FI	
	ication US/0 ON: ON: in-Liang dahl, Lars G Huizhong ON: Lichenas S5-96 ION NUMBER: ATE: 1999-04 ATE: 1999-10 ION NUMBER: ATE: 1997-10 ION NOS: 12 IN Ver. 2.0 In Ver. 2.0 In Ver. 100.0 ION NOS: 12 IN Ver. 100.0 ION NOS: 12 IN Ver. 2.0 IN Ver. 100.0 ION NOS: 12 I	389 367 367 367 368 568 568 568 568 568 568 568 395 395 395 395 395 395 395 395 395 395
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	US/09286690  g ars G. aars G. BER: US/09/286,690 99-04-05 99-10-04 99-10-04 BER: PCT/US97/17811 97-10-03 2.0  succinogenes succinogenes succinogenes 100.0%; Score 1210; DB 3; Length 100.0%; Pred. No. 1.3e-102; 110e.10; Indel:	US-08-640-737-2 US-08-213-419B-19 US-08-213-419B-15 US-08-213-419B-2 US-08-213-419B-4 US-09-620-412C-353 US-08-961-083-2 US-08-481-435-6 US-08-712-072C-2 US-08-484-4531B-3 US-08-444-531B-3 US-08-476-900A-3 US-08-726-320-1 US-08-726-320-1 US-08-726-320-3 US-08-726-321B-3 US-08-404-531B-6 ALIGNMENTS
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ַ <u></u>	Sequence 2, Appli Sequence 15, Appli Sequence 2, Appli Sequence 353, Appli Sequence 353, Appli Sequence 6, Appli Sequence 6, Appli Sequence 16, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 1, Appli Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli

RESULT 2
US-08-103-998-2
; Sequence 2, Application US/08103998
; Patent No. 5470725
; GENERAL INFORMATION:

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RESULT 3
US-09-286-690-8
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                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                   Sequence 8, Application US/09286690 Patent No. 6103511
APPLICANT: L1, Xin-Liang
APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
TITLE OF INVENTION: Lichenase and Coding Sequences
FILE REFERENCE: 55-96
CURRENT APPLICATION NUMBER: US/09/286,690
CURRENT FILING DATE: 1999-04-05
EARLIER APPLICATION NUMBER: US 60/027,882
EARLIER FILING DATE: 1999-10-04
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Best Local :
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APPLICANT: Von Wettst
TITLE OF INVENTION: /
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LENGTH: 239 amino acids
TYPE: amino acid
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PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/773,652
FILLING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC computible
OPERATING SYSTEM: PC-DOS/MS-DOS
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1800 Diagonal Road,
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VENTION: A Thermostable (1,3-1,4)-beta-Glucanase
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Hofemeister, Jurgen
Thomsen, Karl Kristian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.6%; Score 248; DB 1; Length 239; 35.4%; Pred. No. 6.8e-15; tive 27; Mismatches 70; Indels
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RESULT 5
US-09-286-690-9
; Sequence 9, Application US/09286690
; Patent No. 6103511
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CURRENT APPLICATION NUMBER: US/09/286,690
CURRENT FILING DATE: 1999-04-05
EARLIER APPLICATION NUMBER: US 60/027,882
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: PCT/US97/17811
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 243
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LENGTH: 242
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APPLICANT: Ljungdahl, Lars G.
APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
TITLE OF INVENTION: Lichenase and Coding Sequences
FILE REFERENCE: 55-96
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EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 12
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TYPE: PRT
ORGANISM: Bacillus subtilis
                                                                                                                                          194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 Q-LKHTATNQIPTTPGK--IMMNLWNGTGVDEWLGSYNGVN-PLYAHYDWVRYTK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 IDIEFLGKDTTKVQFNYYTNGAG---NHEKIVDLGFDAANAYHTYAFDWQPNSIKWYVDG
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 58; Conserv
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                                                                                                                                                                                                                                                                                                                                                    23 TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI 82
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                                                                                                                                        KHTATTQIPQTPGK--IMMNLWNGAGVDEWLGSYN-GVTPLSRSLHWVRYTK
                                                                                                                                                                                RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 193
                                                                                                                                                                                                                                                                 EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
                                                                                                                                                                                                                                                                                                              TSPSYNKFDCGENRSVQTYGYGLYEVNMKPAKNVGIVSSFFTYTGPT---DGTPWDEIDI 137
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                                                                                                                                                                                                                           EFLGKDTTKVQFNYYTNGVG---NHEKIVNLGFDAANSYHTYAFDWQPNSIKWYVDGQ-L
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33.7%;
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Pred. No. 1.5e-13;
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GENERAL INFORMATION:

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; TYPE: PRT
; ORGANISM: Bacillus polymyxa
US-09-286-690-7
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Best Local Similarity
Watches 61; Conserve
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SEQ ID NO 9
LENGTH: 279
TYPE: PRT
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SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/286,690 CURRENT FILING DATE: 1999-04-05 EARLIER APPLICATION NUMBER: US 60/027,882 EARLIER FILING DATE: 1999-10-04
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EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 12
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TITLE OF INVENTION: L.
FILE REFERENCE: 55-96
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                                        130 IDIEFLGKDTTKVQFNYYTNGVGGH----EKIINLGFDASTSFHTYAFDWQPGYIKWYVDG
140 QEVRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 VYR----GTRNIPVTPGKIMMNLWPGIGVDEWLGRYD-GRTPLQAEYEYVKYY 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 VRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVY 192
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                                                                                                                                                                                                                               Local Similarity
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                                                                                                                      SLTSPANNK-FDCGEYRSTNNYGYGLYEVSMKPAKNTGIVSSFFTYTGPSH---GTQWDE 129
                                                                           VDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IEFLGKDTTKVQFNWYKNGVGG----NEYLHNLGFDASQDFHTYGFEWRPDYIDFYVDGKK 195
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                                                                                                                                                                                                            61;
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35.3%;
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hes 70;
                                                                                                                                                                                                                                                Length 238;
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CURRENT APPLICATION NUMBER: US/09/286,690
CURRENT FILING DATE: 1999-04-05
EARLIER APPLICATION NUMBER: US 60/027,882
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: PCT/US97/17811
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 242
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US-08-103-998-4
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Best Local Similarity
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APPLICANT: Borris
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APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
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ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: FOLEY & L
                                                                                                                                                                                                                                       TITLE OF INVENTION: A Thermostable (1,3-1,4)-beta-Glucanase
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                                                                                                                                                 STREET: 1800 Dias
CITY: Alexandria
                                                                                                             COUNTRY:
                                                                                                                                   STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 VAAAAAALTTNVS-----AKDFSGAELYTLEEVQ-----YGKFEARMKMAAASGTV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKLPL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFHTYGFEWRPDYIDFYVDGKKVYR----GTRNIPVTPGKIMMNLWPGIGVDEWLGRYD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSFFTYTGPS---DNNPWDEIDIEFLGKDTTKVQFNWYKNGVGG---NEYLHNLGFDASQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSTVLEAFTGDISNGKMILTLDREYGGSYPYKSGEYRTKSFFGYGYYEVRMKAAKNVGIV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSMFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -VLKHT---ATTNIPSTPGKIMMNLWNGTGVDSWLGSYNGAN-PLYAEYDWV---KYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62;
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                                                                                                                                                                  E: FOLEY & LARDNER 1800 Diagonal Road,
                                                                                                                USA
                                                                                                                                                                                                                                                          Olsen, Ole
Von Wettstein, Dietrich
                                                                                                                                                                                                                                                                                                                  Hofemeister, Jurgen
                                                                                                                                                                                                                                                                                             Thomsen, Karl Kristian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                   Borriss, Rainer
     PatentIn Release #1.0,
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Pred. No. 9.5e-13;
5; Mismatches 71
                                                                                                                                                                    P.O. Box 299
   Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
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8

CURRENT APPLICATION DATA:

us/08/103,998

APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 43

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; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Orpinomyces sp. PC-2
US-09-286-690-2
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                                                                                                            Query Match
Best Local Similarity 31.6
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09286690 Patent No. 6103511
                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/286,690 CURRENT FILING DATE: 1999-04-05 EARLIER APPLICATION NUMBER: US 60/027,882 EARLIER FILING DATE: 1999-10-04 EARLIER APPLICATION NUMBER: PCT/US97/17811 EARLIER FILING DATE: 1997-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: L1, Xin-Liang
APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
TITLE OF INVENTION: Lichenase and Coding Sequences
FILE REFERENCE: 55-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/773,652
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 RKTEGGOVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 193
81 DIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQ 140
                                           79
                                                                                 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 TSSAYNKFDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGP---AHGTQWDEIDI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                       LTIDRDGSGYTCGEYRTKNYYGYGMFQVNMKPIKNPGVVSSFFTYTGPS---DGTKWDEI 135
                                                                               LTTNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KHTATTQIPAAPGK--IMMNLWNGTGVDDWLGSYNGVN-PIYAHYDWMRYRK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFLGKDTTKVQFNYYTNGAG---NHEKFADLGFDAANAYHTYAFDWQPNSIKWYVDGQ-L 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.2%; Score 222.5;
33.1%; Pred. No. 1.4
                                                                                                                     10.4%; Score 190.5; DB 3; 31.6%; Pred. No. 1.2e-09; tive 17; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25; Mismatches
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nes 79;
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                                                                                                                                                               Length
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                                                                                                                                                               245;
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                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
262 V--FDQ---PFFLILN-VAIGGQWPGNPDATTPF 289
                                172 VGQFDESKLPLFQFINWVKVYKYTPGQGEGGSDF 205
                                                                           220
                                                                                                                                                   163
                                                                                                                                                                                                                            103
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                                                                                                              112 AVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSESAAW 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 AVYTA----YDNIPDTPGKIMMNAWNGIGVDDWLRPFN-GRTNISAYYDWV 238
                                                                                                                                                                        60 SSMFLYQNGSETADGRPWV---EVDI-EVLGKNP----GSFQSNIITGKAGAQKTSEKHH 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/824,707
FILING DATE: 14-April-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 405 Le
CITY: New York
                                                                                                                                                                                                                                                                                                  Local Similarity
les 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                             2 NIKKTAVKSALAVAAAAAALTTNVSAKDFSGAELYTLEEV--QYGKFEARMKMAAASGTV 59
                                                                       GWSFADD--FHTFGIDWTPGEITWLVDGQEYHRVTTADVG-
                                                                                                                                                 SAFWMV -- GANLPD-TPWPTSGEIDIMENVGNAPHEVHGTVHGPGYSGDNGIMGTYQHPQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWV 189
                                                                                                                                                                                                                          NYTTSRVNSALDGQGNLVITALQESDGSYTSARLTTQGNVQPQFGRIEARIQIPRGQGIW 162
                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ferrer, Pau
Diers, Ivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Halkier, Torl
Asenjo, Juan
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hedegaard, Lisbeth
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                                                                                                                                                                                                                                                                                                                                                                                             protein
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                                                                                                                                                                                                                                                                                                                   8.7%;
27.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No. 5919688el enzyme with beta-1,3-glucanase activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4290.204-US
                                                                                                                                                                                                                                                                                                                   Score 159.5; DB 2; Pred. No. 1.1e-06;
                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #1.25 (EPO)
                                                                                                                                                                                                                                                                                                    89;
                                                                                                                                                                                                                                                                                                  Indels 37;
                                                                                                                                                                                                                                                                                                                                   Length 306;
                                                                                                                                                                                                                                                                                                  Gaps
                                                                         261
                                                                                                                                                                                                                                                                                                  11;
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APPLICANT: Ferrer, Pau
APPLICANT: Diers, Ivan
APPLICANT: Holers, Ivan
APPLICANT: Hedegaard, Lisbeth
TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
TITLE OF INVENTION: ACTIVITY
FILE REFERENCE: 4693.204 US
CURRENT APPLICATION NUMBER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER APPLICATION NUMBER: 0427/96
EARLIER APPLICATION DATE: 1996-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SEQ ID NO 2
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                EARLIER APPLICATION NUMBER: 0885/96
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: PCT/DK97/00160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: 0885/96
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: PCT/DK97/00160
EARLIER FILING DATE: 1997-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER FILING DATE: 1996-12-04
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APPLICANT: Diers, Ivan
APPLICANT: Halkier, Torben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 15 SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hedegaard, Lisbeth TITLE OF INVENTION: An Enzyme With TITLE OF INVENTION: Activity FILE REFERENCE: 4693.204-US
                      NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 3.0
                                            EARLIER FILING DATE: 1997-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 DNFDTFDGS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 QYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQSNIITG-- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVYDNGSGS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTQGLRFNLWSSESAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGS----DFTLDWT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGPGYSGGSGITGMYQHPQGWSFADTFHTFAVDWKPGEITWFVDGQQFHRVTRASVG--- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----KAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QYGRIEARIQIPRGQG-IWPAFWMLGGS--FPGTPWPSGEIDIM-ENVG-FEPHRVHGTV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----ANAWV--FDQ---PFFLILN-VAVGGQWPGYPDGTTQLPQQMKVDYV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 263
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10;

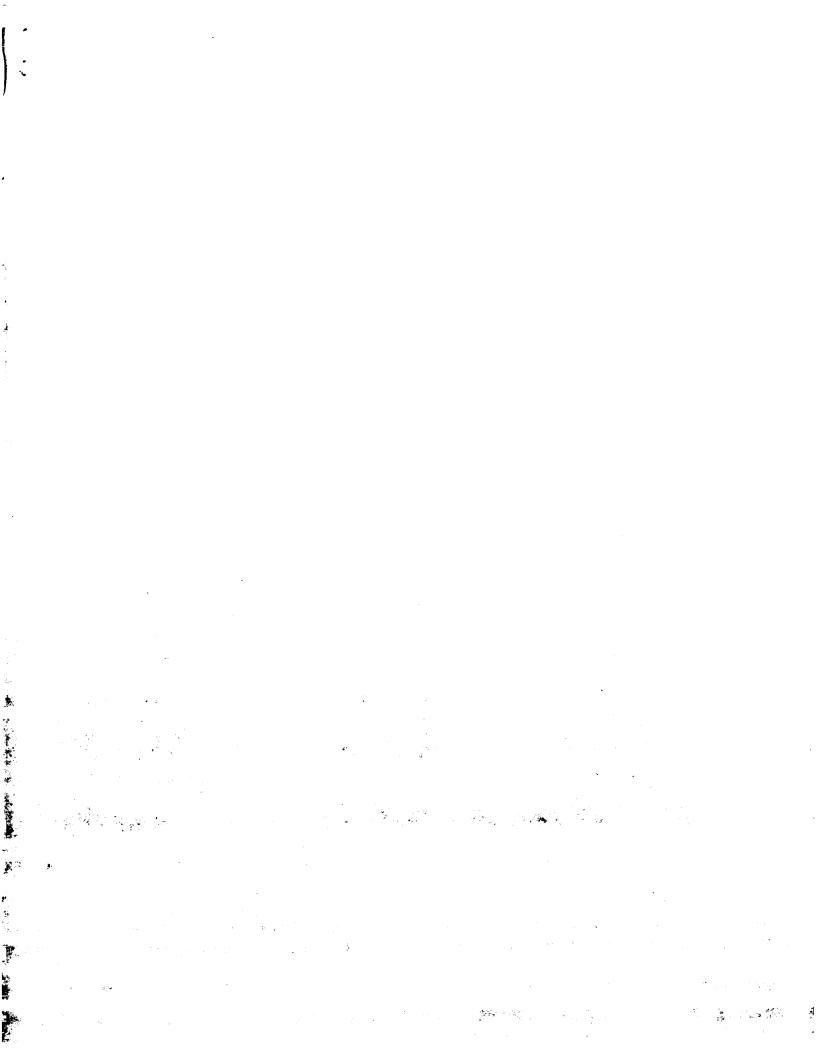
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    Вþ
                                                                                                                                                                                                                                                    ; ORGANISM: Oerskovia xanthineolytica US-09-159-106-13
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US-09-159-106-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-11
                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER FILING DATE: 1996-12-04
EARLIER APPLICATION NUMBER: 0885/96
EARLIER APPLICATION NUMBER: DET/DK97/00160
EARLIER APPLICATION NUMBER: PCT/DK97/00160
EARLIER FILING DATE: 1997-04-14
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 13
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Patent No. 6284509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: An Enzyme TITLE OF INVENTION: Activity FILE REFERENCE: 4693.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ferrer, Pau
APPLICANT: Diers, Ivan
APPLICANT: Halkler, Torben
APPLICANT: Hedegaard, Lisbeth
                                                                                                                                                                                                                                                                                                           LENGTH: 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 RAANGMCVDVPWADPTDGNPVQIVTCSGNAAQTWTRGS---DGT-VRALGKCLDVRDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 QPFFLILNVAVGGQNPGYPDGTTQLPQQMKVDYVRVYDNGSGSSSPGNPGTGLPTGTGAV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 MYQHPQGWSFADTFHTFAVDWKPGEITWFVDGQQFHRVTRASVG------ANAWVFD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 EKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 78; Conserv
88 AELQNYTASRANSALDGQGNLVITARREGDGSYTSARMTTQGKYQPQYGRIEARIQIPRG 147
                                            34 ---ELYTLE----
                                                                                                                                                                  Local Similarity es 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 AELQNYTASRANSALDGQGNLVITARREGDGSYTSARMTTQGKYQPQYGRIEARIQIPRG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 SALVAALTAAAAALAYTVAATSAAAAPGDLLWSDEFDGAAGSAPNPAVWNHETGAHGWGN 87
                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAVKSALAVAAAAALT---TNVSA-----KDFSGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QG-IWPAFWMLGGS -FPGTPWPSSGEIDIMENVGFEPHRVHGTVHGPGYSGGSGI--TG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGTVSSMFLYQNGSEIADGRPWV---EVDI-EVLGKNP----GSFQSNIITGKAGAQKTS 107
                                                                                 SALVAALTAAAAALAVTVAATSAAAAPGDLLWSDEFDGAAGSAPNPAVWNHETGAHGWGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09159106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LDWTDNED-----TFDGS----RWGKGDWTFDGNRVDLTDKNIYSRDG
                                                                                                                                                                Conservative
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21.8%;
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                                                                                                                                                                  34; Mismatches
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                                                                                                                                                                                 Score 141.5; DB 4
Pred. No. 4.9e-05;
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Pred. No. 4.9e-05;
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                                      ----EVOYGKFEARMKMAAA 55
                                                                                                                                                                                                         DB 4;
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                                                                                                                                                                  Indels 109;
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US-08-712-072C-4
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                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                              MOLECULE TYPE: P
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRACMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: gub,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 ANAWY--FDQ---PEFLILN-VAVGGQWPGYPDGTTQLPQQMKVDYVRVYDNGSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 SAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGS----DETLDWTDNFDTFDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: 3.5 INCH 1.44 Mb
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARDS: ASSETS
                                                                    93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 11-SEP-CLASSIFICATION: 435
                                   83
                                                                                                       28
                                                                                                                                                                                                                                                                                                                                                       LENGTH: 276 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bogosian, Elizabeth A. REGISTRATION NUMBER: 39,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                  KDFSGAELYTLEEVQ--YGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWV---EVDI 82
MEHVGFNPDVVHGTVHTKAYNHLLGTQRGGSIR---VPTARTDFHVYAIEWTPEEIRWFV 208
                               -EVLGKNP----GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTV 137
                                                                    REYTSARLVTRGKASWTYGRFEIRARLPSGRGTWPAIWMLPDRQTYGSAY-WPDNGEIDI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYQHPQGWSFADTFHTFAVDWKPGEITWFVDGQQFHRVTRASVG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QG-IWPAFWMLGGS--FPGTPWPSSGEIDIMENVGFEPHRVHGTVHGPGYSGGSGI--TG 202
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                                                                                                                                           44;
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                                                                                                                                                                                                                              gub, Rhodothermus marinus
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VENTION: ENDO-BETA-GALACTOSIDASE
                                                                                                                                           Conservative
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23.7%;
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                                                                                                                                       ; Score 133.5; DB 2;
; Pred. No. 0.00023;
34; Mismatches 85;
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US-08-712-072C-3
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                                                                                                                                                                                     Matches
                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: TWX 710-581-4766 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Elizabet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                           ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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              128 WIPNYVRWIVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSESA-----
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CITY: New York
STATE: NY
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OPERATING SYSTEM: MS-DOS
                                                                                                                                                  20 ALTINVSAKD-----FSGAELYTLEE--VQYGKFEARMKMAAASGTVSSMFLYQNGSEI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII
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ZIP: 10016
                                                                                                                                                                                     Local Similarity es 43; Conserv
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                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bogosian, Elizabeth A. REGISTRATION NUMBER: 39,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                 GTWAASGEIDVMEARGRLPGSVSGTIHFGGQWPVNQSSGGDYHFPEGQTFANDYHVYSVV 243
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                                                                               ADGRPWVEVDI-EVLGKNPGSFQSNIITG----KAGAQKTSEKHHAVSPAADQAFHTYGLE 127
                                                                                                                  AMNDSKSPQDPNRYAQYSSGKINTKDKLSLKYGRVDFRAKLPTGDGVWPALWMLPKDSVY 183
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(212) 286-0854 or 286-0082
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20.4%;
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Pred. No. 0.006;
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Search completed: January 9, 2003, 12:06:35 Job time: 15.7338 secs



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Result
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Maximum Match 100%
Listing first 45 summaries
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Gapop 10.0 ,
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Copyright (c) 1993 - 2003 Compugen
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     2003, 11:49:36;
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US-08-103-998-2
US-09-286-690-10
US-09-286-690-17
US-09-286-690-7
US-09-286-690-7
US-09-286-690-7
US-09-159-106-11
US-09-159-106-2
US-09-159-106-13
US-08-712-072C-4
US-09-159-106-13
US-08-712-072C-3
US-08-580-5458A-4
US-09-262-653A-4
US-09-262-653A-4
US-09-262-653A-4
US-09-262-731-8
US-08-392-828C-2
US-09-330-945-3
US-08-392-828C-37
US-08-392-828C-37
US-08-392-828C-37
US-08-392-828C-37
US-08-392-828C-37
US-08-392-828C-37
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US-09-330-945-37
US-08-712-072C-5
US-09-330-945-37
US-09-330-945-37
US-08-712-072C-5
US-09-330-945-37
US-08-712-073C-5
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Sequence
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Qy Db	Qу	Qy Db	Qу	Que Bes Mat	RESUIUS - 08 S See : Pail : GEE : AII : AII : AII : EE : EE : EE : EE		
Qy 182 FTLDWTDNFDTFDCSRWGKGDWTF 205 	122 TEGGQVSNLTGTQGLRFNLMSSESAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGSD 1 	Qy         62 LGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRK 12           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 2 VSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEV 61	Query Match 82.7%; Score 1103; DB 3; Length 228; Best Local Similarity 100.0%; Pred. No. 3e-106; Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps	· &	ALIGNMENTS	28 109.5 8.2 289 4 US-08-640-737-2 Sequence 2, 1 29 105 7.9 422 2 US-08-712-072C-2 Sequence 2, 1 30 102.5 7.7 395 2 US-08-404-531B-3 Sequence 3, 1 20.5 7.7 395 3 US-08-488-546A-3 Sequence 3, 1 20.5 7.7 1580 4 US-08-726-320-1 Sequence 1, 1 20.5 7.7 1580 4 US-08-726-320-1 Sequence 1, 1 20.5 7.7 1581 4 US-08-726-320-1 Sequence 1, 1 20.5 7.7 1581 4 US-08-726-320-3 Sequence 1, 1 20.5 7.7 1581 4 US-08-726-320-3 Sequence 3, 1 20.5 7.7 1581 4 US-08-726-320-3 Sequence 3, 1 20.5 7.2 1581 4 US-08-208-716-3 Sequence 6, 1 20.5 7.2 1581 3 US-08-404-531B-6 Sequence 6, 1 20.5 7.2 1581 3 US-08-408-546A-6 Sequence 6, 1 20.5 7.2 1581 4 US-09-208-716-4 Sequence 6, 1 20.5 7.2 1581 4 US-09-208-716-4 Sequence 6, 1 20.5 7.2 1582 3 US-08-404-531B-9 Sequence 4, 1 20.5 7.2 1582 3 US-08-404-531B-9 Sequence 9, 1 20.5 7.2 1582 3 US-08-404-531B-9 Sequence 9, 1 20.5 7.2 1582 3 US-08-404-531B-9 Sequence 9, 1 20.5 7.2 1582 3 US-08-408-546A-9 Sequence 9, 1 20.5 7.2 1582 3 US-08-408-546A-9 Sequence 9, 1 20.5 7.2 1582 3 US-08-488-546A-9 Sequence 9, 1 20.5 7.2 1582 3 US-08-488-546
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RESULT 2 US-09-286-690-8 ; Sequence 8, Application US/09286690 ; Patent No. 6103511 ; GENERAL INFORMATION:

APPLICANT: Li, Xin-Liang APPLICANT: Ljungdahl, Lars G. APPLICANT: Chen, Huizhong

Lichenase and Coding Sequences

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US-08-103-998-2
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Best Local :
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              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/773,652
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30307/123
TELECOMMUNICATION INFORMATION:
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CURRENT FILING DATE: 1999-04-05
EARLIER APPLICATION NUMBER: US 60/027,882
EARLIER FILING DATE: 1999-10-04
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 12
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TYPE: PRT
ORGANISM: Bacillus subtilis
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Von Wettstein, Dietrich
TITLE OF INVENTION: A Thermostable (1,3-1,4)-beta-Glucanase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 TKVQFNYYTNGAG---NHEKIVDLGFDAANAYHTYAFDWQPNSIKWYVDGQ-LKHTATNQ 199
                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
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CITY: Alexandria
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TELEPHONE:
                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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Thomsen, Karl Kristian
Olsen, Ole
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US-09-286-690-10
; Sequence 10, Application US/09286690
; Patent No. 6103511
; GENERAL INFORMATION:
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 279
                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: US 60/027,882
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: PCT/US97/17811
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 12
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CURRENT FILING DATE: 1999-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Lichenase and Coding Sequences FILE REFERENCE: 55-96
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Clostridium thermocellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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                                                                                                                                                                119 VRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193
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TOPOLOGY:
                                                                                                                                                                                                                                            59
                                                                                                                                                                                                                                                                              82 REYGGSYPYKSGEYRTKSFFGYGYYEVRMKAAKNVGIVSSFFTYTGPS----DNNPWDEID 138
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nes 61; Conserv
                                                                                                                                                                                                                                                                                                 5 KDFSGAELYTLEEVQ------YGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62
                                                                                                                               VYR----GTRNIPVTPGKIMMNLWPGIGVDEWLGRYD-GRTPLQAEYEYVKYY 243
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                                                                                                                                                                                                                                          IEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---ATANIPSTPGKIMMNLWNGTGVDDWLGSYNGAN-PLYAEYDWV---KYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKDTTKVQFNYYTNGVGGH---EKVISLGFDASKGFHTYAFDWQPGYIKWYVDG-VLKHT
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GY: linear
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35.5%;
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                                                                                                                                                                                                                                                                                                                                                                      Score 231.5; DB 3
Pred. No. 5.2e-16;
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Pred. No. 2.1e-17;
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APPLICANT: Li, Xin-Liang

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                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver.
SEQ ID NO 7
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 7, Application US/09286690 Patent No. 6103511
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SEQ ID NO 10
LENGTH: 243
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CURRENT FILING DATE: 1999-04-05
EARLIER APPLICATION NUMBER: US 60/027,882
EARLIER FILING DATE: 1999-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chen, Huizhong
TITLE OF INVENTION: Lichenase and Coding Sequences
FILE REFERENCE: 55-96
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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    127
                                       140 TKVQFNYYTNGVGGH---EKIINLGFDASTSFHTYAFDWQPGYIKWYVDG-VLKHT---A 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 ATTQIPQTPGK--IMMNLWNGAGVDEWLGSYN-GVTPLSRSLHWVRYTK 242
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                                                                                                                               83
                                                                                                                                                                                                                                    Local Similarity
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VSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 172
                                                                               GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKDTTKVQFNYYTNGVG---NHEKIVNLGFDAANSYHTYAFDWQPNSIKWYVDGQ-LKHT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
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                                                                                                                        FDCGEYRSTNNYGYGLYEVSMKPAKNTGIVSSFFTYTGPSH----GTQWDEIDIEFLGKDT 139
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33.7%; Pred
33.7%; 25;
                                                                                                                                                                                                                             16.9%; Score 225; DB 3; 34.5%; Pred. No. 1.9e-15;
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Pred. No. 6.9e-16;
5; Mismatches 76;
                                                                                                                                                                                                              Mismatches
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CURRENT APPLICATION NUMBER: US/09/286,690
CURRENT FILING DATE: 1999-04-05
EARLIER APPLICATION NUMBER: US 60/027,882
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: PCT/US97/17811
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08103998 Patent No. 5470725
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Best Local Similarity
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APPLICANT: Borris
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APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
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                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 242
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                          APPLICANT: Von Wettstein, Dietrich
TITLE OF INVENTION: A Thermostable (1,3-1,4)-beta-Glucanase
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                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 VYR----GTRNIPVTPGKIMMNLWPGIGVDEWLGRYD-GRTPL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 VRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 IEFLGKDTTKVQFNWYKNGVGG----NEYLHNLGFDASQDFHTYGFEWRPDYIDFYVDGKK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 TTNIPSTPGKIMMNLWNGTGVDSWLGSYNGAN-PLYAEYDWV---KYT
                                                                                                                                                                        COUNTRY:
ZIP: 223
APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                            STREET: 1800 Dia
CITY: Alexandria
STATE: VA
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                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 KDFSGAELYTLEEVQ-----YGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IEVLGKNPGSEQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQE 118
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                                                                                                                                                                                                                                                  1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                  Olsen, Ole
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Hofemeister, Jurgen
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                                                                                                                                                                                                                                                                                                                                                                                        Thomsen,
                                                                                                                                                                                                                                                                        FOLEY & LARDNER
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35.6%;
                                                                                                                                                                                                                                                                                                                                                                                      Karl Kristian
                                                                                                                                                                                                                                                                                                                                                                                                                        Rainer
                                                                            Release #1.0,
                                        US/08/103,998
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Pred. No. 3.6e-15;
                                                                                                                                                                                                                                                    P.O.
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                                                                          Version
                                                                                                                                                                                                                                                    Box 299
                                                                            #1.25
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; SEQ ID NO 2
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Orpinomyces sp. PC-2
US-09-286-690-2
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                                                                                                                                                                                                Matches
                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence 2, Application US/09286690 Patent No. 6103511
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/286,690 CURRENT FILING DATE: 1999-04-05 EARLIER APPLICATION NUMBER: US 60/027,882 EARLIER FILING DATE: 1999-10-04
                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: PCT/US97/17811
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Lichenase and Coding Sequences FILE REFERENCE: 55-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Li, Xin-Liang
APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 30:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
119 VRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWV 166
                                          137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 IPAAPGK--IMMNLWNGTGVDDWLGSYNGVN-PIYAHYDWMRYRK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 TKVQFNYYTNGAG----NHEKFADLGFDAANAYHTYAFDWQPNSIKWYVDGQ-LKHTATTQ 194
                                                                              59
                                                                                                                    83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acids
                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                    5 KDFSGAELYTLEEVQ-----YGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                      IEFLGYDTTKVQFNYYTNGQGHH----EHIHYLGFDASQGFHTYGFFWARNSITWYVDGTA 193
                                                                          IEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQE 118
                                                                                                                  RDGSG---YTCGEYRTKNYYGYGMFQVNMKPIKNPGVVSSFFTYTGPS---DGTKWDEID 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                                                                                                                                                                              56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 16.5%; similarity 33.9%; 56; Conservative 2:
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Pred. No. 5.6e-15;
Pred. No. 5.6e-15;
                                                                                                                                                                                                                                  Length 245;
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RESULT 11
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US-08-824-707-2
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Best Local Similarity 28.5%;
Matches 53; Conservative 28
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APPLICANT: Ferrer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION UMBER: 35,127
REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS: No. 59196880 No. 5919688disk of No. 5919688th America,
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                                                                                                           177 EGGSDF 182
                                                                                                                                            246
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                                                                                                                                                                                                                 188 NVGNAPHEVHGTVHGPGYSGDNGIMGTYQHPQGWSFADD--FHTFGIDWTPGEITWLVDG
                                                                                                                                                                                                                                                                                  131 YTSARLTTQGNVQPQFGRIEARIQIPRGQGIWSAFWMV--GANLPD-TPWPTSGEIDIME 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FITLE OF INVENTION:
                                                                        284 DATTPF 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 VYTA----YDNIPDTPGKIMMNAWNGIGVDDWLRPFN-GRTNISAYYDWV 238
                                                                                                                                                                                                                                   61 VLGKNP----GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 212-00.
TELEPHONE: 212-878-9655
TO NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 14 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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CITY: New York
STATE: New Yor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                   7 FSGAELYTLEEV---QYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWV----EVDI-E
                                                                                                                                                                            QEVRKTEGGQVSNLTGTQGLRFNLWSSESAAWVGQFDESKLPLFQFINWVKVYKYTPGQG 176
                                                                                                                                            QEYHRVTTADVG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 amino acids
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Hedegaard, Lisbeth
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Savva, Demitris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212-867-0123
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Pred. No. 5.5e-08;
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Sequence 2, Application US/09159106
Patent No. 6284509

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TITLE OF INVENTION: An Enzyme with -1,3-Glucanase
TITLE OF INVENTION: ACLIVITY
FILE REFERENCE: 4693-204-US
CURRENT APPLICATION NUMBER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER FILING DATE: 1996-12-04
EARLIER APPLICATION NUMBER: 0885/96
EARLIER APPLICATION NUMBER: 0885/96
EARLIER APPLICATION NUMBER: 07/DK97/00160
EARLIER APPLICATION NUMBER: PCT/DK97/00160
EARLIER FILING DATE: 1996-04-14
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SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 263
TYPE: PRT
ORGANISM: Oerskovia xanthineolytica
US-09-159-106-2
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US-09-159-106-11
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                                                                                SOFTWARE: FastSEQ for Windows Version SEQ ID NO 11
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Best Local Similarity
Matches 49; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER FILING DATE: 1996-12-04
EARLIER APPLICATION NUMBER: 0885/96
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: PCT/DK97/00160
EARLIER FILING DATE: 1997-04-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: An Enzyme With -1,3-Glucanase TITLE OF INVENTION: Activity FILE REFERENCE: 4693.204-US
                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Halkier, Torben APPLICANT: Hedegaard, Lisbeth
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ferrer, Pau APPLICANT: Diers, Ivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Halkier, Torben APPLICANT: Hedegaard, Lisbeth
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APPLICANT: Diers, Ivan
APPLICANT: Halkier, Torben
                ORGANISM: Oerskovia xanthineolytica
                                        LENGTH: 435
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTQGLRFNLWSSESAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGS----DFTLDWT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QYGRIEARIQIPRGQG-IWPAFWMLGGS--FPGTPWPSGEIDIM-ENVG-FEPHRVHGTV 136
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Pred. No. 4.2e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: An Enzyme With -1,3-Gluc TITLE OF INVENTION: Activity FILE REFERENCE: 4693.204-US CURRENT APPLICATION NUMBER: US/09/159,106 CURRENT FILING DATE: 1998-09-23 EARLIER APPLICATION NUMBER: 0427/96 EARLIER FILING DATE: 1996-12-04 EARLIER FILING DATE: 1996-12-04 EARLIER FILING DATE: 1996-12-04 EARLIER FILING DATE: 1996-08-23 EARLIER FILING DATE: 1996-08-23 EARLIER APPLICATION NUMBER: PCT/DK97/00160
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 13
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Best Local Similarity
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 628450
                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ferrer, Pau APPLICANT: Diers, Ivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER FILING DATE: 1997-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Halkier, Torben APPLICANT: Hedegaard, Lisbeth
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Oerskovia kanthineolytica
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 303
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 287
                                    187 TDNFDTFDGS 196
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                                                                                                                                                                                   71
                                                                                                                                                                                                                                          19 QYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWV---EVDI-EVLGKNP----GSFQ
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VRVYDNGSGS
                                                                                                                                              GPGYSGGSGI--TGMYQHPQGWSFADTFHTFAVDWKPGEITWFVDGQQFHRVTRASVG--
                                                                                                                                                                                                                   QYGRIEARIQIPRGQG-IWPAFWMLGGS--FPGTPWPSSGEIDIMENVGFEPHRVHGTVH 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWV---EVDI-EVLGKNP----GSFQ 70
                                                                                                                                                                                 SNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ANAWVFCQPFFLILNVAVGGQWPGYPDGTTQLPQQMKVDYVRVYDNGSGSSSP
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                                                                                                         TGTQGLRFNLWSSESAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGS----DFTLDW 186
                                                                                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09159106
                                                                                                                                                                                                                                                                                              Conservative
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24.6%;
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                                                                                                                                                                                                                                                                                              25;
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                                                                                                                                                                                                                                                                                                              Score 140.5; DB 4
Pred. No. 1.5e-06;
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Pred. No. 1.4e-06;
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                                                                                                                                                                                                                                                                                                                               DB 4;
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RESULT 15
US-08-712-072C-3
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US-08-712-072C-4
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BOGOSIBN, ELIZABETH A.
RECISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 63475/97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEFX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08712072C Patent No. 5925541 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US/08/712,072C
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NOTA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
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TITLE OF INVENTION: ENDO-BETA-GALACTOSIDASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amster, Rothstein & Ebenstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                        209
                                                                                                                                                                                              115
                                                                                                                                                                                                                                152 MEHVGFNPDVVHGTVHTKAYNHLLGTQRGGSIR---VPTARTDFHVYAIEWTPEEIRWFV 208
                                                                            269 VRVYRW 274
                                                                                                                  166 VKVYKY 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                             93 REYTSARLVTRGKASWTYGRFEIRARLPSGRGTWPAIWMLPDRQTYGSAY-WPDNGEIDI 151
                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 23.7 es 44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COPOLOGY:
                                                                                                                                                        DDSLYYRFPNERLTDPEADWRHWPFDQPFHLIMNIAVGGAWGGQQGVDPEAFPAQLVVDY 268
                                                                                                                                                                                          DGQEVRKTEGGQVSNLTG-----TQGLRFNLWSSESAAWVGQ--FDESKLPLFQFINW 165
                                                                                                                                                                                                                                                                     -EVLGKNP----GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTV 114
                                                                                                                                                                                                                                                                                                                                                 KDFSGAELYTLEEVQ--YGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWV---EVDI 59
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                                                                                                                                                                                                                                                                                                                                                                                     10.0%; Score 133.5; DB 2; 23.7%; Pred. No. 7e-06; tive 34; Mismatches 85;
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Search completed: January Job time: 10.7593 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 286-0854 or 286-0082 TELEX: TWX 710-581-4766 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BOGOSIAN, ELIZABETH A.
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 63475/97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE:
ORIGINAL SOURCE:
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MOLECULE TYPE: pe
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ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Elizabet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: YU ...
CITY: New York
TMATE: NY
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TITLE OF INVENTION: ENDO-BETA-GALACTOSIDASE
NUMBER OF SEQUENCES: 13
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ANTI-SENSE: NO
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                                                                               306 IPATMQVDYVRVYKF
                                                                                                                                                               260 KVTNQQ-------WYSTAAPNNPNAPFDEPFYLIMNLAVGGNFDGGRTPNASD 305
                                                                                                                                                                                                                                                                                                                       140 YSSGKINTKDKLSLKYGRVDERAKLPTGDGVWPALMMLPKDSVYGTWAASGEIDVMEARG 199
                                                                                                                   157 LPLFQFINWVKVYKY 171
                                                                                                                                                                                                  121 KTEGGQVSNLTGTQGLRFNLWSSESA-----
                                                                                                                                                                                                                                          200 RLPGSVSGTIHFGGQWPVNQSSGGDYHFPEGQTFANDYHVYSVVWEEDNIKWYVDGKFFY 259
                                                                                                                                                                                                                                                                                  64 KNPGSFQSNIITG----KAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVR 120
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Maximum Match 10
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq
                                                                                                                             Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/1/paa/US
2: /cgn2_6/ptodata/1/paa/US
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4: /cgn2_6/ptodata/1/paa/US
6: /cgn2_6/ptodata/1/paa/US
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11: /cgn2_6/ptodata/1/paa/U
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/paa/US07_COMB.pep:*
/cgn2_6/ptodata/1/paa/US080_COMB.pep:*
/cgn2_6/ptodata/1/paa/US081_COMB.pep:*
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	-09-791-537-3709	-09-791-537-7988	-09-791-537-6482	-09-791-537-10381	-09-791-537-10381	-09-791-537-10335	-09-791-537-10335	-09-791-537-10335	-09-791-537-10334	9-791-537-106	-09-791-537-10332	-09-791-537-7627	-09-791-537-8887	-60-360-039-2199	-09-791-537-7284	-09-791-537-6704	-09-791-537-3044	-09-791-537-4890	-09-791-537-1038	-60-096-409-1480	-10-179-131-985	-09-248-796-148	-60-385-568-2	-09-791-537-1867	-09-791-537-8855	09-791-537-1169	-09-791-537-5010	-09-791-537-3043	-09-791-537-31771	-09-791-537-1173	-09-791-537-7988	-09-791-537-7345	09-791-537-10332	-09-791-537-1033	-09-791-537-2	09-791-537-1322	-09-791-537-691	9-463-862A-	-09-791-537-3
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09654652A
GENERAL INFORMATION:
APPLICANT: SHYUR, LIE-FEN
APPLICANT: CHEW, JUI-LIN
APPLICANT: YANG, NING-SUN
TITLE OF INVENTION: A TRUNCATED FORM OF FIBROBACTER SUCCINOGENES 1, 3-1,
TITLE OF INVENTION: 4-BETA-D-GLUCANASE WITH IMPROVED ENZYMATIC ACTIVITY
TITLE OF INVENTION: THERMO-TOLERANCE
FILE REFERENCE: 4910-8
                                                                                                                                                                                            SEQ ID NO 3
LENGTH: 349
TYPE: PRT
                                                                            Query Match
Best Local S
Matches 349
                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/654,652A
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                          ORGANISM: Fibrobacter succinogenes
                                                                            Local Similarity
mes 349; Conserv
                1 MNIKKTAVKSALAVAAAAAALTTNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVS 60
MNIKKTAVKSALAVAAAAAALTTNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVS
                                                                              Conservative
                                                                                             100.0%;
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                                                                          Score 1824; DB 20;
Pred. No: 1.3e-151;
Mismatches 0;
                                                                                                                Length 349;
                                                                          0;
                                                                          Gaps
60
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                                                                          0;
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Result No.

Score

Query Match Length

DB

ID

Description

SUMMARIES

1824 1824 1340 1328 272.5 266.5

100.0 100.0 73.5 72.8 14.9 14.6

349 349 267 248 214 259

US-09-654-652A-3 US-09-791-537-30441 US-09-654-652A-2 US-09-654-652A-1 US-09-791-537-145019 US-09-791-537-106873

Sequence 3, Appli Sequence 30441, A Sequence 2, Appli Sequence 1, Appli Sequence 145019, Sequence 106873,

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Sequence 30441, Application US/09791537

Sequence 30441, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Blonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 30441
LENGTH: 349
TYPE: PRT
ORGANISM: Fibrobacter succinogenes
US-09-791-537-30441
                        RESULT 3
US-09-654-652A-2
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Best Local Simi
Matches 349;
     Sequence 2, Application
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              US/09654652A
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GENERAL INFORMATION:
APPLICANT: SHYUR, LIE-FEN
APPLICANT: YANC, JUI-LIN
APPLICANT: YANC, NING-SUN
TITLE OF INVENTION: A TRUNCATED FORM OF FIBROBACTER SUCCINOGENES 1, 3-1,
TITLE OF INVENTION: THERMO-TOLUCANASE WITH IMPROVED ENZYMATIC ACTIVITY AND
TITLE OF INVENTION: THERMO-TOLERANCE
FILE REFERENCE: 4910-8
CURRENT APPLICATION NUMBER: US/09/654,652A
CURRENT APPLICATION NUMBER: US/09/654,652A
CURRENT FILING DATE: 2000-09-05
NUMBER OF SED ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 267
TYPE: PRT
ORGANISM: Artificial Sequence
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; OTHER INFORMATION: with enhanced activity and thermal stability
US-09-654-652a-2
                                                                                                                         US-09-654-652A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-654-652A-1
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                                                                                                                                                                                                 TITLE OF INVENTION: A TRUNCATED FORM OF FIBROBACTER SUCCINGENES 1, 3-1,
TITLE OF INVENTION: 4-BETA-D-GLUCANASE WITH IMPROVED ENZYMATIC ACTIVITY AND
TITLE OF INVENTION: THERMO-TOLERANCE
FILE REFERENCE: 4910-8
CURRENT APPLICATION NUMBER: US/09/654,652A
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 248
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
CONTROL TO THE CONTROL OF THE CO
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Query Match
Best Local Similarity
Matches 247; Conserv
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SHYUR, LIE-FEN APPLICANT: CHEN, JUI-LIN APPLICANT: YANG, NING-SUN
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                                                                                                                                              Description of Artificial Sequence: with enhanced activity and thermal:
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Score 1328; DB 20;
; Pred. No. 4.2e-108
0; Mismatches 0;
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Pred. No. 4.1e-109;
0; Mismatches 1;
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RESULT 6
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US-09-791-537-145019
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                                                                                           Sequence 106873, Application US/09791537 GENERAL INFORMATION:
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SEQ ID NO 145019
LENCTH: 214
TYPE: PRT
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Best Local Similarity
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FAPILICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
APPLICANT: Danzer, Joseph TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER TITLE OF INVENTION: METHODS OF USE THEREOF FILE REFERENCE: 261/210
                                              APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Josep
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                                                                                                                                                                                                                                                                                                                    TKVQFNYYTNGVGGH----EKVISLGFDASKGFHTYAFDWQPGYIKWYVDG-VLKHT---A
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                                                                                                                                                                                                                                                                                                                                                                                  FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGP---AHGTQWDEIDIEFLGKDT 57
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LENGTH: 252
TYPE: PRT
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Best Local (
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; ORGANISM: Brevibacillus brevis US-09-791-537-106873
                       Sequence 1, Application US/09463862A
GENERAL INFORMATION:
APPLICANT: Hillen, Wolfgang
APPLICANT: Maurer, Karl-Heinz
TITLE OF INVENTION: New Beta-Glucanase from
FILE REFERENCE: H2081PCT/US
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 106873
LENGTH: 259
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
CURRENT APPLICATION NUMBER: US/09/463,862A
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                                                                                                                                                                                                                                                                          206 ----TENIPQTPQKIMMNLWPGVGVDGWTGVFDGDNTPVYSYYDWV----RYTP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SARNYKAGELRTNDFYHYGLFEVSMKPAKVEGTVSSFFTY-TGEWDWDGDPWDEIDIEFL 148
                                                                                                                                                                                                                                                                                                                        EGGQVSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP
                                                                                                                                                                                                                                                                                                                                                                                                                       GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SARNYKAGELRTNDFYHYGLFEVSMKPAKVEGTVSSFFTY-TGEWDWDGDPWDEIDIEFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKDTTRIQENYFTNGVGG----NEFYYDLGFDASESFNTYAFEWREDSITWYVNGEAVHTA
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35.8%; Pred. No. 1.86
tive 24; Mismatches
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Pred. No. 1.6
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hes 74;
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CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: DE 197 32 751.6
PRIOR FILING DATE: 1997-07-30
PRIOR FILING DATE: 1997-07-21
PRIOR PLICATION NUMBER: PCT/EP98/04564
PRIOR FILING DATE: 1998-07-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 308
TYPE: PAT
ORGANISM: Bacillus alkalophilus DSM 9956
US-09-463-862A-1
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APPLICANT: Dobe, Derek
APPLICANT: Dobze, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOPTWARE: Patentin version 3.0
SEQ ID NO 6910
LENGTH: 208
LENGTH: 208
RESULT 10
US-09-791-537-132244
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Best Local Similarity
Matches 77; Conserv
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                                                                                                          161
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                                                                                                                                                                                                111 TANIPSTPGKIMMNLWNGTGVDDWLGSYNGAN-PLYAEYDWV---KYT----SNGSVF--
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                                                                                                        -WEPK-SYFNPSTWEKADGYSNGGVFNCTWRANNVNFTNDGKLKLGLT 206
                                                                                                                                                                                                                                                                                    TKVQFNYYTNGVGGH----EKVISLGFDASKGFHTYAFDWQPGYIKWYVDG-VLKHT---A 110
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                                                                                                                                                  DWTDNFDTFDGSRWGKGDWTFDGNRVDLT--DKNI-YSRDGMLILALT 252
                                                                                                                                                                                                                                        VSNLTGTOG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGSDFTL 207
                                                                                                                                                                                                                                                                                                                                                                            FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGP---AHGTQWDEIDIEFLGKDT 57
                                                                                                                                                                                                                                                                                                                                                                                                                      FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTRVQFNYFTNGVG----NNEHYHELGFDASESFNTYAFEWRPESISWYVNGELVYTA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EYKAGELRTNQFYQYGLFEVNMKPAKSTGTVSSLFTY-TGPWDWDNDPWDEIDIEFLGKD 154
                                                                                                                                                                                                                                                                                                                                GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.1%; Score 256.5; DB 2
33.8%; Pred. No. 8.7e-14;
htive 29; Mismatches 95
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US-09-791-537-27063
: Sequence 27063, Application US/09791537
: GENERAL INFORMATION:
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US-09-791-537-132244
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APPLICANT: Debe, Derek
APPLICANTON: THEE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION ONDER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 27063
LENGTH: 242
TYPE: PRT
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 132244
LENGTH: 394
TYPE: PRT
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                                                                         Matches
                                                                                                                   Query Match
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APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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                                                                     y Match 13.7%; Score 250.5; DB 21; Local Similarity 35.5%; Pred. No. 3.6e-13; hes 61; Conservative 25; Mismatches 75;
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58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSAPASSSSVPASSSSVPASSSSAFVPPSSSSATNAIHGM 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPLIEYYVVDSWGTYRPTGTYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQ
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                                                                       Indels 11;
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RESULT 12
US-09-791-537-103347
; Sequence 103347, Application US/09791537
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                                                                                                       ; ORGANISM: synthetic construct
US-09-791-537-103324
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 103347
                                   Best Loc
Matches
                                                                                                                                                     SOFTWARE: PatentIn version 3.0 SEQ ID NO 103324 LENGTH: 239
                                                                                                                                                                                                                                                                                                                                                            Sequence 103324, Application US/09791537 GENERAL INFORMATION:
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APPLICANT: Danzer, JOseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                         APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                           FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bionomix, Inc.
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TYPE: PRT
                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 RKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83
23 TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI 82
                                   Local Similarity es 62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSPSYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVLGKNPGSFQSNIITGKAGAQKTSEKHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFLGKDTTKVQFNYYTNGAG----NHEKFADLGFDAANAYHTYAFDWQPGYIKWYVDG-VL
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                                   Conservative
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                                 13.6%; Score 248; DB 2
35.4%; Pred. No. 6e-13;
Live 27; Mismatches
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Pred. No. 4.9e-13;
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                                                                 Length 239;
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US-09-791-537-73450
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                                                                                 ; ORGANISM: Bacillus subtilis US-09-791-537-79889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Bacillus subtilis US-09-791-537-73450
                                                                                                                SOFTWARE: PatentIn version
SEQ ID NO 79889
LENGTH: 242
TYPE: PRT
                                                Query Match
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                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63;
                Conservative
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THEE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION UMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 73450
LENGTH: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 79889, Application US/09791537 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 VDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q-LKHTATNQIPTTLGK--IMMNLWNGTGVDEWLGSYNGVN-PLYAHYDWVRYTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QEVRKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTSPAYNK-FDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPT---DGTPWDE 133
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                      Score 248;
Pred. No.
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Pred. No. 6.1e-13;
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  6.1e-13;
cches 75;
                                                 DB 21;
                                            Length 242;
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Result
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Perfect score:
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          1824
268.5.5
265.5.5
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endo-1,3(4)-beta-9
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endo-beta-1,3-1,4-
hybrid-endo-beta-1
UTR2 protein - Rhi
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hypothetical prote
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81 81 81 41 41 01	<pre>lery Match log.0%; Score 1824; DB 2; Length 349; sst Local Similarity 100.0%; Pred. No. 1.5e-122; sttches 349; Conservative 0; Mismatches 0; Indels 0; G  1 MNIKKTAVKSALAVAAAAALTTNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVS                                      </pre>	l sinase (EC 3.2.1.73) - Fibrobacter succinogenes ies: Fibrobacter succinogenes: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change sion: A44507 e: DNA sequence of a Fibrobacter succinogenes mixed-linka rence number: A44507; MUID:90299807; PMID:2193918 ssion: A44507 us: preliminary cule type: DNA crease succinogenes mixed-linka session: A44507 us: preliminary cule type: DNA dues: 1-349 <tea> dues: 1-349 <tea> creferences: EMBL:M33676; NID:g148575; PIDN:AAA24896.1; ords: g1ycosidase; hydrolase; polysaccharide degradation</tea></tea>	
30 24 4	349; 0; Gaps 0; anasgrvs 60           anasgrvs 60            vspandqa 120           vspandqa 120                   vspandqa 120           gqfpeskt 180	e 08-Oct-1999 age beta-glucanase (1,3	xyloglucan endo-1, probable xylogluca xyloglucan endo-1, xyloglucan endo-1, xyloglucan endo-1, probable membrane xyloglucan endo-1, licheninase (EC 3. xyloglucan endo-1, beta-glucanase (im endo-1,3(4)-beta-gucanase (im endo-1,3(4)-beta-gucanase (im xyloglucan endo-1, xyloglucan

RESULT 2
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H84053
endo-beta-1,3-1,4 glucanase (licheninase) bglS [imported] - Bacillus halodurans
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001
C:Accession: H84053

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A;Molecule type: nucleic acid
A;Residues: 1-252 <LOU>
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A;Title: Characterization, cloning and sequencing of a thermostable endo-(1,3-1,4) beta. A;Reference number: A48378; MUID:93159752; PMID:7763386
A;Accession: A48378
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodu: A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H84053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: A48378
R;Louw, M.E.; Reid, S.J.; Watson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Bacillus brevis
C; Date: 01-Dec-1993 #sequer
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A48378
licheninase (EC 3.2.1.73) - Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-851 <STO>
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                                                                                                                                                                                            SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL
---TENIPQTPQKIMMNLWPGVGVDGWTGVFDGDNTPVYSYYDWV----RYTP
                                      EGGQVSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP 196
                                                                                  GKDTTRIQFNYFTNGVGG----NEFYYDLGFDASESFNTYAFEWREDSITWYVNGEAVHTA
                                                                                                                         GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 145
                                                                                                                                                                  SARNYKAGELRTNDFYHYGLFEVSMKPAKVEGTVSSFFTY-TGEWDWDGDPWDEIDIEFL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALDEEESGDDNEEEPVEEVEEEPAEDEEVSVRPIGSAIYETFNTFNEDIWSIAHGWT-NG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTTNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRVDLT--DKNIYSRDGMLILALTRKGQESFNGQVPRDDEPA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVHTA----TENIPQTPQKIMMNLWPGVGVDEWTGVFDGDNTPLHADYEWV---RYTPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVRKTEGGQVSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP-- 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIEFLGKDTTRIQFNYFTNGVGG----NEFYYDLGFDASESFNTYAFEWREDSITWYVNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQ 140
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                                                                                                                                                                                                                                                                        Similarity
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29.48;
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Pred. No. 9.2e-12;
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A;Cross references: EMBL: 246862; NID: 9599673; A;Cross references: EMBL: 246862; NID: 9599674
A;Cross references: EMBL: 246862; NID: 9599673; A;Cross references: EMBL: 268862; NID: 9599673; A;Cross references: EMBL: 258862; NID: 9599673; A;Cross references: PID: 9599673; A;Cross references
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A; Reslidues: 1-23',5',25-82',5',84-242 <TEZ>
A; Cross-references: DDBJ:D00518; NID:g216243; PID
A; Experimental source: strain Y-25; Clone pLE100
R; Yuuki, T.; Tezuka, H.; Yabbuchi, S.
Agric. Blol. Chem. 53, 2341-2346, 1989
A; Title: purification and some properties of two
A; Reference number: A90027
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Rucleic Acids Res. 12, 5355-5367, 1984

A;Title: The DNA sequence of the gene and genetic control sites for the example of the sequence of the gene and genetic control sites for the example of the gene and genetic control sites for the example of the gene and genetic control sites for the example of the gene and genetic control sites for the example of the gene and genetic control sites for the example of the gene and genetic control sites for the example of the gene and genetic control sites for the example of the general sites of the general 
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C:Species: Bacillus subtilis
C;Date: 30-Jun-1988 #sequence_revision 13-Mar-1998 #text_change 16-Jun-2000
C:Accession: I40370; B6594; A22914; A90026; A90027; JU0110
R:Wolf, M.; Geczi, A.; Simon, O.; Borriss, R.
Microbiology 141, 281-290, 1995
C;Superfamily: licheninase
C;Keywords: extracellular protein; glycosidase;
F;1-28/Domain: signal sequence #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: the amino C; Genetics:
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Agric. Biol. Chem. 53, 2335-2339, 1989
A:Title: Construction of a beta-glucanase hyperproducing
A:Reference number: A90026
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                                                                                                                                                                                                                                                                                                                C; Function:
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A;Molecule type: DNA
A;Residues: 1-242 <RES>
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C;Species: Bacillus sp.
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 22-Jun-1999
C;Accession: 140453; S23688
R;Tabernero, C.; Coll, P.M.; Fernandez-Abalos, J.M.; Perez, P.; Santamaria, R.I.
Appl. Environ. Microbiol. 60, 1213-1220, 1994
A;Reference number: 140453; MUID:94288605; PMID:7517127
A;Reference number: 140453; MUID:94288605; PMID:7517127
                                                                                                                         licheninase (EC 3.2.1.73) beta - Bacillus amyloliquefaciens N;Alternate names: 1,3-1,4-beta-D-glucan 4-glucanohydrolase; beta-glucanase C;Species: Bacillus amyloliquefaciens C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 (C;Accession: A29091 R;Hofemeister, J.; Kurtz, A.; Borriss, R.; Knowles, J. Gene 49, 177-187, 1986
                                                                      Gene 49, 177-187, 1986
A; Title: The beta-glucanase
A; Reference number: A91564;
A; Accession: A29091
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C;Superfamily: licheninas
C;Keywords: glycosidase;
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 A;Cross-references:
A;Experimental source
                                   A; Molecule type: DNA
A; Residues: 1-239 <HOF>
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GB:M15674; NID:g143009; PIDN:AAA87323.1; ce: strain BE20/78
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Pred. No. 1.5e-10;
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type:
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C;Species: Clostridium thermocellum
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C;Accession: S23498; S22137
R;Schimming, S; Schwarz, W.H.; Staudenbauer, W.L.
Eur. J. Biochem. 204, 13-19, 1992
A;Title: Structure of the Clostridium thermocellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     xylanase, beta(1,3-1,4)-glucanase - Ruminococcus flavefaciens
C;Species: Ruminococcus flavefaciens
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_chan
C;Accession: A36910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: bglA
C;Superfamily: licheninase
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:S61204; NID:g385910; PIDN:AAB26620.1; PID:g385911
A;Note: sequence extracted from NCBI backbone (NCBIN:131871, NCBIP:131872)
C;Superfamily: endo-1.4-beta-xylanase homology; Thermotoga xylanase A amino-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Flint, H.J.; Martin, J.; McPherson, C.A.; Daniel, A.S.; Zhang, J. Bacteriol. 175, 2943-2951, 1993
A; Reference number: S23498;
A; Accession: S23498
                                                                                                                                                                                                                                                    licheninase (EC 3.2.1.73) licB precursor - Clostridium the N;Alternate names: beta-1,3-1,4-glucanase licB; lichenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;42-239/Domain: endo-1,4-beta-xylanase homology <xy1> F;259-401/Domain: Thermotoga xylanase A amino-terminal repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-802 <FLI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: A bifunctional enzyme, with separate xylanase and beta(1,3-1,4)-glucanase A;Reference number: A36910; MUID:93259938; PMID:8491715 A;Accession: A36910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 KHTATTQIPAAPGK--IMMNLWNGTGVDDWLGSYNGVN-PIYAHYDWMRYRK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YSGGEFRINNFYHYGYYECSMQAMKNDGVVSSFFTYTGPS---DDNPWDEIDIEILGKNT 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI 82
                                                                                                                                                                                                                                                                                                                                                                                                                           TQDIPKTPGKIMMNAWPGLTVDDWLKAFN-GRTPLTAHYQWVTYNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFLGKDTTKVQFNYTINGAG----NHEKFADLGFDAANAYHTYAFDWQPNSIKWYVDGQ-L 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSPSYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE----GTPWDEIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TQVQFNYYTNGQGKH---EKLYDLGFDSSEAYHTYGFDWQPNYIAWYVDGREVYRA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
59; Conserv
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                             MUID:92155194; PMID:1740123
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Pred. No. 3.7
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                                                                                    beta-1,3
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A;Gene: 11cB
C;Superfamily: licheninase licB; Clostridium cellulase repeat homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-334/Product: licheninase #status predicted <MAT>
F;273-296/Domain: Clostridium cellulase repeat homology <CCR1>
F;308-331/Domain: Clostridium cellulase repeat homology <CCR2>
                                                                                                                                                                                                                                                                                                                                                                              A:Molecule type: DNA
A;Residues: 1-243 <LLO>
A;Cross-references: EMBL:X57279; NID:g39558; PIDN:CAA40547.1;
C;Superfamily: licheninase
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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Eur. J. Biochem. 197, 337-343, 1991
A;Title: Molecular cloning, express
A;Reference number: S15388; MUID:91
A;Accession: S15388
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RESULT 10
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      licheninase (EC 3.2.1.73) - Bacillus licheniformis N;Alternate names: endo-beta-1,3-1,4-D-glucanase; lichenase
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Best Local
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                                                      KHTATTQIPQTPGK--IMMNLWNGAGVDEWLGSYN-GVTPLSRSLHWVRYTK
                                                                                            RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 193
                                                                                                                                        EFLGKDTTKVQFNYYTNGVG---NHEKIVNLGFDAANSYHTYAFDWQPNSIKWYVDGQ-L 193
                                                                                                                                                                              EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
                                                                                                                                                                                                                                                            TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVNRDG-RIDSTDLTMLKR 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REYGGSYPYKSGEYRTKSFFGYGYYEVRMKAAKNVGIVSSFFTYTGPS---DNNPWDEID 138
                                                                                                                                                                                                                    TSPSYNKFDCGENRSVQTYGYGLYEVNMKPAKNVGIVSSFFTYTGPT---DGTPWDEIDI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DWTFDGNRVDLTDKNIYSR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NPTPTPTIAPSTPTNPNLPLKGDVNGDGHVNSSDYSLFKRYLLRVIDRFPVGDQS----VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDFSGAELYTLEEVQ-----YGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IEFLGKDTTKVQFNWYKNGVGG---NEYLHNLGFDASQDFHTYGFEWRPDYIDFYVDGKK 195
                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                       12.8%; Score 233.5; DB : 33.7%; Pred. No. 1.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression and MUID: 91224124;
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                                                                                                                                                                                                                                                                                                      26; Mismatches
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Pred. No. 1.4e-09;
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PMID:2026156
                                                                                                                                                                                                                                                                                                                                            DB 1;
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A;Cross references: EMBL:x55959; NID:g296715; PIDN:CAA39426 R; Hahn, M.; Heinemann, U. submitted to the Brookhaven Protein Data Bank, December 199 A;Reference number: A67074; PDB:IMAC A;Contents: annotation; X-ray crystallography, 2.3 angstrom A;Note: recombinant form with residues 26-41 from Bacillus R;Keitel, T.; Simon, O.; Borriss, R.; Heinemann, U. Proc. Natl. Acad. Sci. U.S.A. 90, 5287-5291, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
S11927
                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: endo-beta-1,3-1,4-glucanase; lic
C;Species: Bacillus macerans
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
C;Accession: S11927
R;Borriss, R.; Buettner, K.; Maentsaelae, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable membrane protein YGR189c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein G7553
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
C;Accession: S64507
                                                                                                                                                                                                                                                            A; Reference number: S11927;
A; Accession: S11927
                                                                                                                                                                                                                                                                                          Mol. Gen. Genet. 222, 278-283, 1990
A; Title: Structure of the beta-1, 3-1, 4-glucanase
A; Reference number: S11927, MUID: 91109712; PMID:
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A;Map position: 7R
C;Keywords: transmembrane protein
F;6-22/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-237 <BOR>
                                                                                                                                                                                                                                           A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-507 <ARR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S64507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              licheninase (EC 3.2.1.73) precursor [validated] -
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                                                                                                                                                                     PIDN:CAA39426.1;
                                                                        2.3 angstroms,
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                                                ns, residues 26-37,'p',39-2 amyloliquefaciens expresse
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A;Description: catalyzes the hydrolysis of 1,4-beta-D-glucosidic C;Superfamily: licheninase C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;1-25/Domain: signal sequence #status predicted <PRO> F;26-237/Product: licheninase #status experimental <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Bacillus polymyxa
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      licheninase (EC 3.2.1.73) precursor - Bacillus polymyxa
N;Alternate_names: endo-beta-1,3-1,4-glucanase; lichenase
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S19012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X57094; NID:g48815; PIDN:CAA40379.1; PID:g48817C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-238 <GOS>
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A;Contents: annotation; X-ray crystallography, 2.3 angstroms
A;Note: recombinant form with residues 26-41 from Bacillus amyloliquefaciens expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S19012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Gosalbes, M.J.; Perez-Gonzalez, J.A.; Gonzalez, R.; Navarro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: S19012
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Best Local
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                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                   QEVRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 195
                                                                                                                                                                                                           SLTSPANNK-FDCGEYRSTNNYGYGLYEVSMKPAKNTGIVSSFFTYTGPSH---GTQWDE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KHT---ATANIPSTPGKIMMNLWNGTGVDDWLGSYNGAN-PLYAEYDWV---KYT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI 82
                                                                                                                                                       VDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDG 139
                                                                                                                                                                                                                                                   ALTTNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVE 79
                                            -VLKHT---ATTNIPSTPGKIMMNLWNGTGVDSWLGSYNGAN-PLYAEYDWV---KYT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary
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                                                                                                                              IDIEFLGKDTTKVQFNYYTNGVGGH---EKIINLGFDASTSFHTYAFDWQPGYIKWYVDG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFLGKDTTKVQFNYYTNGVGGH----EKVISLGFDASKGFHTYAFDWQPGYIKWYVDG-VL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60;
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                                                                                                                                                                                                                                                                                          Score 227.5; DB 1
Pred. No. 4.4e-09;
26; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 228; DB 1
Pred. No. 4e-09;
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                                                                                                                                                                                                                                                                                            17;
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C; Superfamily: licheninase
                       A; Gene: CAC2807
                                            C; Genetics:
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Matches
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RESULT

13

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A;Cross-references: EMBL:X58392
R;Zverlov, V.V.; Velikodvorskaya, G.A.
Biotechnol. Lett. 12, 811-816, 1990
A;Title: Cloning the Clostridium thermocellum
A;Cross-references: GB:AED01437; P1
A;Experimental source: Clostridium
                                                                                 A; Molecule type: DNA
                                                                                                                                        A; Reference number: A96900; A; Accession: D97245
                                                                                                                                                                .; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4338, 2001
A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                       R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova,
                                                                                                                                                                                                                                                                                                                     endo-1,3(4)-beta-glucanase family 16 [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C;Accession: D97245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: licheninase
C;Keywords: glycosidase; nydrolase; polysaccharide degradation
F;1-27/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: X58392
A; Note: the nucleotide sequence was
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
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A; Accession: S18726
A; Status: preliminary; nucleic acid
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A; Residues: 1-242 <ZVE1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:Zverlov, V.V.; Laptev, D.A.; Tishkov, V.I.; Velikodvorskaja, G.A. Biochem. Biophys. Res. Commun. 181, 507-512, 1991
Biochem. Rucleotide sequence of the Clostridium thermocellum laminarinase A;Reference number: JS0611; MUID:92095946; PMID:1755832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: JS0611; S18726
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                                                            A; Residues: 1-246 < KUR>
                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;28-242/Product: endo-1,3(4)-beta-glucanase #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRTPL 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DFHTYGFEWRPDYIDEYVDGKKVYR----GTRNIPVTPGKIMMNLWPGIGVDEWLGRYD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSFFTYTGPS----DNNPWDEIDIEFLGKDTTKVQFNWYKNGVGG----NEYLHNLGFDASQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSTVLEAFTGDISNGKMILTLDREYGGSYPYKSGEYRTKSFFGYGYYEVRMKAAKNVGIV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAAAAAALTTNVS-----AKDFSGAELYTLEEVQ-----YGKFEARMKMAAASGTV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSMFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
PIDN:AAK80751.1; PID:g15025848; GSPDB:GN00168 um acetobutylicum ATCC824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 242;
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                                                                                                                                                                                                     Solvent-Producing Bacterium
                                                                                                                                                                                                                                                                                          Zeng, Q.; Gibson,
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В
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A:Map position: linear chromosome
C:Superfamily: licheninase
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-263 < KUR>
A;Cross-references: GB:AE008689; PIDN:AAL44856.1; PID:g17742502; GSPDB:GN00187
A;Cross-references: GB:AE008689; DIDN:AAL44856.1; PID:g17742502; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: AB3055
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AB3055
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AB3055
AB3055-1,4-beta-glycanase exoK [imported] - Agrobacterium tumefaciens (strain C58, Dup C;Species: Agrobacterium tumefaciens C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
Search completed: January Job time: 18.5613 secs
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Best Local Similarity 33.7
Matches 58; Conservative
                                                                                                                                              147 GGQVSNLT----GTQGLRFNLWSSESAA-WVGQF 175
                                                                                                                                                                                                          146 NTGKVQLNQYIAAKGG----NEKLVPVEGGADAGFNDYAFVWEPQRLRYYVNGKLVH--- 198
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                                                                                                       199 -- EVTDETKIPQNAQKIFFSLWGTDTLKDWMGKF 230
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                                                                                                                                                                                                                                                                                                            89 RNFACGEIQTKGRYRYGTYEARMKAATGSGLNSAFFTYIGPT---DKKPHDEIDFEVLGK 145
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les 54; Conserv
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                                                                                                                                                                                                                                                              NPGSFQSN-IITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTE 146
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    11.3%; Score 206; DB 2; Length 263; 35.1%; Pred. No. 1.7e-07; ative 26; Mismatches 56; Indels
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                        2003, 12:19:01
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Maximum DB seq
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Perfect score:
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1824
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   GenCore version (c) 1993 - 2003
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GUB_BACLI
YG46_YEAST
GUB_PAEMA
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P34127 dictyosteli	085465 bacillus ag			P49012 phanerochae	-				Q45760 bacillus th		Q9kka3 r outer mem

ALIGNMENTS

## GUB\_FIBSU STANDARD; PRT; 349 AA. P17989; 01-NOV-1990 (Rel. 16, Created) 01-NOV-1990 (Rel. 16, Last sequence update) 15-JUL-1990 (Rel. 38, Last annotation update) Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase) (1,3-1,4-beta-D-glucan 4-glucanchydrolase) (Mixed linkage beta-glucanase) (Lichenase). Fibrobacter succincgenes (Bacteroides succincgenes). Bacteria; Fibrobacter/Acidobacteria group; Fibrobacter group; SEQUENCE FROM N.A., AND SEQUENCE STRAIN=Isolate S85; MEDLINE=90299807; PubMed=2193918; NCBI\_TaxID=833; AND SEQUENCE OF 28-57.

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CC Query Match
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Matches 349; Conserv ACT\_SITE
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REPEAT Teather R.M., Erfle J.D.;

"DNA sequence of a Fibrobacter succinogenes mixed-linkage beta-glucance (1,3-1,4-beta-D-glucan 4-glucanchydrolase) gene.";

J. Bacteriol. 172:3837-3841(1990).

-!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.

-!- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES. Hydrolase; SIGNAL This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). CHAIN EMBL; M33676; AAA24896.1; PIR; A44507; A44507. PROSITE; Pfam; PF00722; HSSP; nterPro; P23904; 1AJK 00722; Glyco\_hydro\_16; 1. PS01034; GLYCOSYL\_HYDROL\_F16; IPR000757; Glyco\_hydro\_16 Glycosidase; 100.0%; ilarity 100.0%; Conservative 28 79 83 271 271 278 285 292 ÃĀ; 37737 MW; Signal; Repeat. .' BETA-GLUCANASE.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
5 x 7 AA TANDEM REPEATS OF P-X.
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4.
5. Score 1824; DB 1; Pred. No. 1.9e-123; ; Mismatches 0; 16DC4F5BDEFC578A CRC64; P-X-S-S-S-X 349;

0;

1.9e-123;

Length Indels

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Gaps

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GUB_BACABR
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                 Pfam; PF00722; Glyco_hydro_16.
PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLHYDRLASE16.
Hydrolase; Glycosidase; Signal.
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01-JUN-1994 (Rel. 29, Createu)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
01-JUN-1994 (Rel. 29, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
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P37073;
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                                                                                                                                                                                           EMBL; M84339;
HSSP; P23904;
                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-93159752; PubMed-7763386;
LOUW M.E., Reid S.J., Watson T.G.;
"Characterization, cloning and sequencing of."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus brevis."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. Microbiol. Biotechnol. 38:507-513(1993).
FUNCTION: HYDROLYSES B-GLUCANS CONTAINING MIXED BETA-1,3 AND BETA-1,4 LINKAGES. THIS ENZYME IS THERMOSTABLE; ITS OPTIMAL TEMPERATURE IS NEAR 65-70 DEGREES CELSIUS.
CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.
MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILAR TO LICHENASE OF GERMINATING BARLEY. SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES
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  BETA-GLUCANASE
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RESULT 3
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ACT_SITE
SEQUENCE
                                                         Wolf M., Geczi A., Simon O., Borriss R.; "Genes encoding xylan and beta-glucan hydrolysing subtilis: characterization, mapping and constructideficient in lichenase, cellulase and xylanase."; Microbiology 141:281-290(1995).
                                                                                                                                                                     "Sequencing of a 65 kb region of containing the lic and cel loci, covering the gnt-sacXY region."; Microbiology 142:3113-3123(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1987 (Rel. 05, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
BGLS OR BGL OR LICS OR N15B.
                                                                                                                                                                                                                                                                                Tezuka H., Yuuki T., Yabuuchi S.;
Tezuka H., Yuuki T., Yabuuchi S.;
"Construction of a beta-glucanase hyperproducing Bacii using the cloned beta-glucanase gene and a multi-copy norin Riol. Chem. 53:2335-2339(1989).
                                                                                                                                                                                                                                                                                                                                                                                 Murphy N., McConnell D.J., Cantwell B.A.; and The DNA sequence of the gene and genetic cexcreted B. subtilis enzyme beta-glucanase. Nucleic Acids Res. 12:5355-5367(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus subtilis.
Bacteria; Firmicutes;
NCBI_TaxID=1423;
                       STRAIN-BR15
                                   SEQUENCE
                                                                                                          MEDLINE=95219081; PubMed=7704256; Wolf M., Geczi A., Simon O., Borr
                                                                                                                                     STRAIN=168
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                     Miwa Y., Fujita Y.;
                                                                                                                                                                                                                                             MEDLINE=97124196; PubMed=8969509;
                                                                                                                                                                                                                                                            STRAIN=168
                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                STRAIN-HL-25;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                  Yoshida K.-I., Shindo
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=84272222;
        MEDLINE=96178961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKDTTRIQFNYFTNGVGG----NEFYYDLGFDASESFNTYAFEWREDSITWYVNGEAVHTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity
63; Conserv
                                   OF 1-6
                                                                                                                                                                                                                                                          / BGSC1A1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259
Stuelke J.,
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                                   FROM
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          PubMed=8606172;
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146
29960
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Gertz S.,
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ene and genetic control
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Pred. No. 2.9e
24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTON DONOR
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                                                                                                                                                                                                                                  Η.,
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                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillaceae;
Krueger
                                                                                                                                                                                                                                  Seki S.,
                                                             and construction of str. nd xylanase.";
                                                                                                                                                                                              Bacillus
creation
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                                                                                                                                                                                                                                  Fujimura M.,
                                                                                                                                                                                              subtilis
of a 177
Krieg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus
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IPR000757; Glyco\_hydro\_16

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RESULT
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P27051;
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ACT_SITE
ACT_SITE
                                 Querol E.;
Submitted
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PROSITE;
                                                                                                                                                                                                            Beta-glucanase precurso (1,3-1,4-beta-D-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00404; Dockerin_1; 2.
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
                                                                           "Molecular cloning, expression and nucleotide sequence of the endo-beta-1,3-1,4-D-glucanase gene from Bacillus licheniformis Predictive structural analyses of the encoded polypeptide."; Eur. J. Blochem. 197:337-343(1991).
                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-91224124; PubMed-2026156;
                                                                                                                                                                     Bacteria; Firmicutes; NCBI_TaxID=1402;
                                                                                                                                                                                            Bacillus licheniformis
                                                                                                                                                                                                                           01-AUG-1992 (Rel. 23, Cre
01-AUG-1992 (Rel. 23, Las
01-NOV-1997 (Rel. 35, Las
Beta-glucanase precursor
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MEDLINE=92362869;
           MUTAGENESIS
                                                        REVISIONS
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                                                                                                                        Lloberas J., Perez-Pons J.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IEFLGKDTTKVQFNWYKNGVGG---NEYLHNLGFDASQDFHTYGFEWRPDYIDFYVDGKK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REYGGSYPYKSGEYRTKSFFGYGYYEVRMKAAKNVGIVSSFFTYTGPS---DNNPWDEID
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PS01034; GLYCOSYL, HYDROL, F16;

PS00018; EF_HAND; UNKOWN_2.

PS00448; CLOS_CELLULOSOME_RPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 30.9
30; Conservative
                                 (JUL-1991)
                                                                                                                                                                                                                                                                                                                                                                                                            Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334
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136
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PubMed=1354172;
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30.9%;
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Last annotation update)
sor (EC 3.2.1.73) (Endo-beta-1,3-1,4
n 4-glucanohydrolase) (Lichenase).
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                                                                                                                                                                               Bacillales;
                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal; Repeat.
                                                                                                                                                                                                                                                                                                                                           325
                                                                                                                                                                                                                                                                                                                                                               243
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                                 EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTON DONOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
PRO/THR-RICH (LINKER).
2 X 24 AA ADDDO
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Pred. No. 5.
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                                                                                                                        Querol E.;
                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                               Bacillaceae;
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                                 databases
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                                                                                                                                                                                                                          glucanase)
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3).
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83

EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV

TSPSYNKFDCGENRSYQTYGYGLYEVNMKPAKNYGIVSSFFTYTGPT---DGTPWDEIDI

137

81

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8
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                                             Query Match
Best Local
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"Crystal structure of Bacillus licheniformis 1,3-1,4-beta-D-glucan 4-
glucanohydrolase at 1.8-A resolution.";
FEBS Lett. 374:221-224(1995).
                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glucanohydrolase from B. licheniformis as determined mutagenesis.";
                                                                                                        MUTAGEN
MUTAGEN
                                                                                                                                    MUTAGEN
MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.
-i- MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANG SIMILAR TO LICHENASE OF GERMINATING BARLEY.
-i- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         site-directed mutagenesis
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Hydrolase: Glycosidase; Signal; 3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00722; Glyco_hydro_16; PRINTS; PR00737; GLHYDRLASE16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       pdb; 1GBG; 07-DEC-95.
InterPro; IPR000757; Glyco_hydro_16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Planas A., Juncosa M., Lloberas J., Querol E.;
"Essential catalytic role of Glu134 in endo-beta-1,3-1,4-D-glucan 4-
                                                                                                                                                                   MUTAGEN
                                                                                                                                                                                                 MUTAGEN
                                                                                                                                                                                                                                                                                                        MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Juncosa M., Pons J., Dot T., Querol E., Planas A.;
"Identification of active site carboxylic residues in I
licheniformis 1,3-1,4-beta-D-glucan 4-glucanohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
                                            Local
 23
TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S15388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X57279; CAA40547.1;
                                             Similarity
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                                                                                         AA;
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                                             33
                                            . 7%;
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                             26;
                                            Score
Pred.
                                                                                                      PROTON
                                                                                                                                                                                                                                                                                                                                                                 BETA-GLUCANASE
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                             Mismatches
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2. 3% OF WILD-TYPE ACTIVITY.
2. 3% OF WILD-TYPE ACTIVITY.
3. 3% OF WILD-TYPE ACTIVITY.
4. 15% OF WILD-TYPE ACTIVITY.
5. 0.2% OF WILD-TYPE ACTIVITY.
5. 0.2% OF WILD-TYPE ACTIVITY.
6.5% OF WILD-TYPE ACTIVITY.
                          e 233.5; Db 1,
No. 6.1e-10;
                                                                                                                                                                                                                                                                                                                                    DONOR
                                                                                        & OF WILD-TYPE ACTI
CHANGE IN ACTIVITY
D9AAD609A5 CRC64;
                             Indels
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RKTEGGOVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK

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EFLGKDTTKVQFNYYTNGVG----NHEKIVNLGFDAANSYHTYAFDWQPNSIKWYVDGQ-L

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YG46_YEAST
ID YG46_Y
AC P53301
DT 01-OCT
DT 01-OCT
DT 01-OCT
DT 01-NOV
DE Hypoth
GN YGR189
OS Sacchae
OX NCB1_T
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01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
Hypothetical 52.8 kDa protein in BUB1-HIP1
YGR189C OR G7553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "DNA sequence analysis of a 23,002 bp DNA fragment of the of Saccharomyces cerevisiae chromosome VII."; Yeast 13:357-363(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00722; Glyco_hydro_16;
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Saccharomycetales; Saccharomycetaceae; Saccharomyces
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                                                     172
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234 AGGETNYNDAPFTMYIEKVIVTDYSTGKKYTYGDQSGSW-ESIEADGGSIYGRYDQAQE-
                                                                                                       180
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                                  V-GOFDESKLPLFQFINWVKVYKYTPGQGEGGSDFTLDWTDNFDTFDGSRWGKGDWTFDG
                                                                                                  LDWAMDKTTWYLDGESVR-----VLSNTSSEGYPQSPMYLMMGIWAGGDPDNAAGTIEW
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X99074; CAA67525.1; -.
P23904; 1AJK.
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87; Conserv
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P23904;
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Hoej P.B., Condron R., Traeger J.C., McAuliffe J.C., Stone B.A.;
"Identification of glutamic acid 105 at the active site of Bacil.
amyloliquefaciens 1.3-1,4-beta-D-glucan 4-glucanohydrolase using
epoxide-based inhibitors.";
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Paenibacillus macerans (Bacillus macerans).
Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
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01-JUN-1994 (Rel.
15-JUL-1998 (Rel.
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                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hahn M., Keitel T., Heinemann U.;
"Crystal and molecular structure at 0.16-nm resolution of the hybrid Bacillus endo-1,3-1,4-beta-D-glucan 4-glucanohydrolase H(Al6-M).";
Eur. J. Biochem. 232:849-888(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glucanase."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-91109712; PubMed-2274030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.
-!- MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-96028129; PubMed-7588726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93281743; PubMed=8099449; Reitel T., Simon O., Borriss R., Heinemann U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTAGENESIS OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular and active-site structure of a Bacillus
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                                                                                                                        X55959; CAA39426.1;
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31-MAR-95.
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el. 29, Last sequence update)
el. 36, Last annotation update)
precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
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Bacillus
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RESULT 4
GUB_BACAM
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EMBL; D00518; BAA00405.1; -
EMBL; D83026; BAA11697.1; -
EMBL; Z46862; CAA86922.1; -
EMBL; Z28340; CAA82195.1; -
EMBL; Z99124; CAB15943.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Bacteriol. 178:1971
[6]
SEQUENCE OF 29-63.
Yuuki T., Tezuka H., Y
GUB_BACAM
P07980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
ACT_SITE
ACT_SITE
DISULFID
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VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"LicT, a
the BglG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A22914; LXBS.
PIR; JU0110; JU0110.
HSSP; P27051; 1GBC;
Subtilist; BG10476; bgls.
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       + +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hyperproducing strain, Bacillus sur
Agric Biol Chem 53:2341-2346(198
-i- CATALYTIC ACTIVITY: Hydrolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Purification and some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                          191
                                                                                                                                                                                      140
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                                                                                                                                                                                                                                                                                  80
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MISCELLANEOUS: THE SEQUENCE OF STRAIN 168 IS SHOWN.
SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in beta-D-glucans containing 1,3- and 1,4-bonds. SUBCELLULAR LOCATION: Secreted.
MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE
                                                                                                                                     Q-LKHTATNQIPTTPGK--IMMNLWNGTGVDEWLGSYNGVN-PLYAHYDWVRYTK 241
                                                                                                                                                                                                                                                                         VDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDG 139
                                                                                                                                                                                                                                                                                                                                                                        ALTTNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVE 79
                                                                                                                                                                                 QEVRKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 193
                                                                                                                                                                                                                                                                                                                            ALTSPAYNK-FDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPT---DGTPWDE
                                                                                                                                                                                                                               IDIEFLGKDTTKVQFNYYTNGAG----NHEKIVDLGFDAANAYHTYAFDWQPNSIKWYVDG
                                                                                                                                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS01034; GLYCOSYL_HYDROL_F16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycosidase;
1 28
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133
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Them. 53:2341-2346(1989).

ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic containing 1,3- and 1,4-bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178:1971-1979(1996)
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                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          properties of two enzymes from Bacillus subtilis HL-25.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 248; DB 1;
Pred. No. 5.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTON DONOR (BY SIMILARITY).
BY SIMILARITY.
A -> S (IN STRAIN HL-25).
A -> S (IN STRAIN HL-25).
P -> L (IN STRAIN C120).
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                        PRT;
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                        239
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Best Local
      053317;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
11-NOV-1997 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Xylanase/beta-glucanase precursor [Includes: Endo-1,4-beta-xylanase (EC 3.2.1.8) (Xylanase); Endo-beta-1,3-1,4 glucanase (EC 3.2.1.73)
(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hofemeister J., Kurtz A., Borriss R., Knowles J., "The beta-glucanase gene from Bacillus amyloliquefaciens extensive homology with that of Bacillus subtilis."; Gene 49:177-187(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AuG-1988 (Rel. 08, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1988 (Rel.
01-AUG-1988 (Rel.
01-JUN-1994 (Rel.
                                                                                                                    ZYND_
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus amyloliquefaci
Bacteria; Firmicutes; F
XYND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
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HSSP; P27051; 1GBG.
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MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILAR TO LICHENASE OF GERMINATING BARLEY. SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES
                                                                                                                 _RUMFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                          KHTATTQIPAAPGK--IMMNLWNGTGVDDWLGSYNGVN-PIYAHYDWMRYRK
                                                                                                                                                                                                                      RKTEGGOVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 193
                                                                                                                                                                                                                                                                                                                                           TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
                                                                                                                                                                                                                                                    EFLGKDTTKVQFNYYTNGAG----NHEKFADLGFDAANAYHTYAFDWQPNSIKWYVDGQ-L
                                                                                                                                                                                                                                                                                EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
                                                                                                                                                                                                                                                                                                               TSPSYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDI 133
                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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134
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239
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                                                                                                                   STANDARD;
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Bacillales;
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                                                                                                                                                                                                                                                                                                                                                                      Score 242.5; DB 1
Pred. No. 1.4e-10;
7; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
A76A64268A7AAA0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOPHILE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BETA-GLUCANASE.
                                                                                                                   PRT;
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. <sub>P</sub>B
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Best Local
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InterPro: IPR00137; GH_1.
InterPro: IPR001137; GH_1.
InterPro: IPR001137; GH_21.
InterPro: IPR007757; GLYco_hydro_11; 1.
Pfam: PF00457; GLYco_hydro_16; 1.
Pfam: PF02018; CBM_4_9; 1.
Pfam: PF02018; CBM_4_9; 1.
PRINTS: PR00911; GLHYDRLASE11.
PRINTS: PR00737; GLHYDRLASE16.
PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
PROSITE: PS00777; GLYCOSYL_HYDROL_F16; 1.
PROSITE: PS01034; GLYCOSYL_HYDROL_F16; 1.
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ACT_SITE
                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; S61204;
HSSP; P23904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glucanase domains, encoded by flavefaciens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-
                  691 TOVOFNYYTNGQGKH---
                                                                                              634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     xylan degradation; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93259938; PubMed-8491715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruminococcus flavefaciens.
                                                90 GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 149
                                                                                                                30 FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: CONTAINS TWO CATALYTIC DOMAINS WITH XYLANASE AND ENDOBETA-1,3-1,4 GLUCANASE ACTIVITIES.
CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G (FAMILY 11 OF GLYCOSYL HYDROLASES). SIMILARITY: IN THE C-TERMINAL SECTION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: Xylan degradation. SECTION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linkages in xylans.
                                                                                        YSGGEFRTNNFYHYGYYECSMQAMKNDGVVSSFFTYTGPS---DDNPWDEIDIEILGKNT 690
                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Firmicutes; Clostridia; Clostridiales; Lachnospiraceae;
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                EKLYDLGFDSSEAYHTYGFDWQPNYIAWYVDGREVYRA---
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Pred. No. 6e-1
Pred. Mismatches
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                                                                                                                                                                                                                                                                    POLY-THR
                                                                                                                                                                                                                                                                                                                         C (BETA-GLUCANASE).
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                    POLY-THR.
                                                                                                                                                                                                                                                                                                          POLY-THR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               XYLANASE/BETA-GLUCANASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycosidase;
                                                                                                                                                                                                                                                2880A689647284AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (XYLANASE).
                                                                                                                                                                                      6e-10
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HSSP;

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RESULT 6
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Beta-
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                                                                          EMBL; X63355; CAA44959.1; EMBL; X58392; CAA41281.1; PIR; S23498; S23498. PIR; JS0611; JS0611. PIR; S18726; S18726.
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P29716; P370
01-APR-1993
                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extrement the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                      entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=F7;
Zverlov V.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in Escherichia coli; the properties of Biotechnol. Lett. 12:811-816(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biotechnol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zverlov V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92095946; PubMed-1755832;
Zverlov V.V., Laptev D.A., Tishkov V.I., Velikodvors)
"Nucleotide sequence of the Clostridium thermocellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lichenases joined to cellulases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta-1,3-1,4-glucanase. A catalytic region homologous to lichemases joined to the reiterated domain of clostridial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schimming S., Schwarz W.H., Staudenbauer W. Structure of the Clostridium thermocellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-ATCC 27405 / DSM 1237;
MEDLINE-92155194; PubMed-1740123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beta-glucanase precursor (EC 3.2.1.73). (Enc (1,3-1,4-beta-D-glucan 4-glucanohydrolase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994 (Rel.
01-FEB-1996 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning the Clostridium thermocellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        744 TQDIPKTPGKIMMNAWPGLTVDDWLKAFN-GRTPLTAHYQWVTYNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.
SUBUNIT: MAY FORM PART OF A MULTIENZYME COMPLEX (CELLULOSOME).
DOMAIN: A 24 RESIDUES DOMAIN IS REPEATED TWICE IN THIS ENZYME AS WELL AS IN OTHER C.THERMCCELLUM CELLULUSOME ENZYMES. THIS DOMAIN MAY FUNCTION AS THE BINDING LICAND FOR THE SL COMPONERY.
SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biochem. 204:13-19(1992).
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29, Last sequence update)
29, Last sequence update)
. 33, Last annotation update)
recursor (EC 3.2.1.73), (Endo-beta-1,3-1,4 glucanase)
recursor (EC 3.2.1.73), (Lichenase) (Laminarinase).
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                                                                                                                                                                                                                                                                  agreement (See
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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                                                                                   : //gn2_6/ptodata/1/paa/US083_COMB.pep: *
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://gn2_16/ptodata/1/paa/US085_COMB.pep: *
://gn2_16/ptodata/1/paa/US085_COMB.pep: *
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://gn2_16/ptodata/1/paa/US086_COMB.pep: *
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/cgn2_6/ptodata/1/paa/US07_COMB.pep:*
/cgn2_6/ptodata/1/paa/US080_COMB.pep:*
/cgn2_6/ptodata/1/paa/US081_COMB.pep:*
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265.5 18.5 252 21 US-09-791-537-32335 Sequence 32335, 257.5 17.9 308 18 US-09-791-537-6210 Sequence 6910, 250.5 17.4 394 21 US-09-791-537-117361 Sequence 6910, 247.5 17.2 276 21 US-09-791-537-117361 Sequence 27063, 245.5 17.1 242 21 US-09-791-537-117361 Sequence 27063, 245.5 17.1 242 21 US-09-791-537-103347 Sequence 173450, 245.5 17.1 242 21 US-09-791-537-103347 Sequence 79889, 245.5 17.0 239 21 US-09-791-537-103347 Sequence 103344 242.5 16.9 802 21 US-09-791-537-103347 Sequence 103344 242.5 16.9 802 21 US-09-791-537-103347 Sequence 20107, 242.5 16.9 802 21 US-09-791-537-10334 Sequence 30103, 244.5 16.5 344 21 US-09-791-537-10347 Sequence 103344 242.5 16.9 802 21 US-09-791-537-10347 Sequence 20107, 242.5 16.9 802 21 US-09-791-537-10347 Sequence 30103, 244.5 16.3 239 21 US-09-791-537-10345 Sequence 81007, 234.5 16.3 239 21 US-09-791-537-10381 Sequence 81007, 234.5 16.3 239 21 US-09-791-537-103817 Sequence 103748, 235.5 16.4 21 US-09-791-537-103817 Sequence 81679, 235.5 16.4 21 US-09-791-537-103817 Sequence 107048, 236.5 15.7 214 21 US-09-791-537-103817 Sequence 707048, 236.5 15.7 239 21 US-09-791-537-103817 Sequence 81071, 236.5 15.7 239 21 US-09-791-537-103817 Sequence 81071, 236.5 15.7 239 21 US-09-791-537-103350 Sequence 103345 Sequence 103357 Sequence 103358 Sequence 103357 Sequence 103
8.5 252 21 US-09-791-537-3235 Sequence 3235, 7.9 308 18 US-09-463-862A-1 Sequence 610, App. 7.9 208 21 US-09-791-537-6210 Sequence 611, App. 7.9 214 21 US-09-791-537-117361 Sequence 117361 224 21 US-09-791-537-117361 Sequence 2706. 21 US-09-791-537-717361 Sequence 2707. 276 21 US-09-791-537-73450 Sequence 73450, 7.1 242 21 US-09-791-537-73450 Sequence 73450, 7.1 242 21 US-09-791-537-73450 Sequence 2706. 239 21 US-09-791-537-10334 Sequence 103344 Sequence 103344 Sequence 103344 Sequence 2708. 239 21 US-09-791-537-10324 Sequence 103344 Sequence 2708. 239 21 US-09-791-537-10350 Sequence 2708. 239 21 US-09-791-537-103817 Sequence 2708. 239 21 US-09-791-537-103817 Sequence 2708. 239 21 US-09-791-537-103817 Sequence 2708. 239 21 US-09-791-537-103345 Sequence 2708. 239 21 US-09-791-537-103350 Sequence 103345 Sequence 103345 Sequence 103345 Sequence 2708. 239 21 US-09-791-537-103350 Sequence 103345
52 21 US-09-791-537-32335 Sequence 32335,   81 US-09-463-862A-1 Sequence 610,   94 21 US-09-791-537-610 Sequence 6110,   95 21 US-09-791-537-117361 Sequence 132244   96 21 US-09-791-537-117361 Sequence 117361   97 21 US-09-791-537-71450 Sequence 27063,   97 21 US-09-791-537-71450 Sequence 103347   97 21 US-09-791-537-10324 Sequence 103347   97 21 US-09-791-537-10324 Sequence 103347   97 21 US-09-791-537-10324 Sequence 103347   98 21 US-09-791-537-10343 Sequence 103347   99 21 US-09-791-537-10343 Sequence 103349   90 21 US-09-791-537-10343 Sequence 116925 Sequence 10324   90 21 US-09-791-537-103817 Sequence 88552 Sequence 88552 Sequence 103349   91 US-09-791-537-103817 Sequence 103817   92 1 US-09-791-537-103817 Sequence 67048,   93 21 US-09-791-537-103817 Sequence 67048,   94 21 US-09-791-537-103350 Sequence 103345   95 21 US-09-791-537-103350 Sequence 103346   96 21 US-09-791-537-103350 Sequence 103346   97 21 US-09-791-537-103350 Sequence 103350 Sequence 103350   97 21 US-09-791-537-103814 Sequence 103350
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-09-791-537-3235 Sequence 3235,   -09-463-862A-1 Sequence 510,   -09-791-537-6910 Sequence 510,   -09-791-537-13224 Sequence 132244 Sequence 132244 Sequence 132244 Sequence 132244 Sequence 13234-109-791-537-27063 Sequence 73450,   -09-791-537-103324 Sequence 103347 Sequence 103347-09-791-537-10324 Sequence 5107-791-537-10325 Sequence 10324-109-791-537-103817 Sequence 10326-109-791-537-103817 Sequence 10326-109-791-537-103817 Sequence 10326-109-791-537-103817 Sequence 10326-109-791-537-103320 Sequence 10326-109-791-537-103320 Sequence 76270,   -09-791-537-103350 Sequence 103357-09-791-537-103357 Sequence 103357-09-791-537-103357 Sequence 103357-09-791-537-103814 Sequence 103357-09-791-537-3485 Sequence 103357-09-791-537-4487-09-248-796-14807-09-248-79
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אַלְּמֶלְ מִּלְּמֶלְ מִּלְ מִלְּמִלְ מִּלְ מִלְּמֶלְ מִּלְ מִּלְּמְלְ מִלְּמְלְ מְלְמִלְ מִלְּמְלְ מִלְּמְלְ מִוּלְם מִינְיִים מְּלְמִים מְלְּמְלְתְּיִם מְלְמִים מִינְיִים מִינְיים מִינִים מִינְיים מִינְיים מִינְיים מִּינְיים מִּינְיים מִינְיים מִינִים מִינְיים מִינְיים מִינְיים מִּינְיים מִּינְיים מִּינְים מִּים מִּינְים מִּינְים מִּינְים מִּינְים מִּינְים מִינְים מִּינְים מִינְים מִּינְים מִּינְים מִּינְים מִּינְים מִינְים מִינְים מִינְים מִינְים מְינִים מְינִים מְינִים מְינִים מְינִים מְינִים מְינִים מְינְים מְינִים מְינִים מְינִים מְינִים מְינִים מְינִים מְינִים מְינִים מְינְים מְינִים מְינְים מְינִים מְינְים מְינִים מְינְיים מְינְיים מְינְים מְינְים מְינְים מְינִים מְינְיים מְינְים מְינִים מְינְיים מְינְיים מְינְיים מְינְיים מְינְיים מְינְיים מְינְיים מְינְיים מְינְיים מְיים מְיים מְינִים מְינְיים מְיים מְיי

## ALIGNMENTS

US-09-654-652A-2

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CURRENT APPLICATION UNMBER: US/09/654,652A
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 11
SOTTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 267
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                 ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Modified
; OTHER INFORMATION: with enhanced activity and thermal stability
US-09-654-652A-2
                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09654652A

GENERAL INFORMATION:
APPLICANT: SHYUR, LIE-FEN
APPLICANT: YANG, NING-SUN
APPLICANT: YANG, NING-SUN
APPLICANT: YANG, NING-SUN
APPLICANT: YANG, NING-SUN
TITLE OF INVENTION: 4-BETA-D-GLUCANASE WITH IMPROVED ENZYMATIC ACTIVITY AND
TITLE OF INVENTION: THERMO-TOLERANCE
FILE REFERENCE: 4910-8

CIUDEDENIM APPLICANT: WANG
THERMO-TOLERANCE
    Matches 267;
                         Query Match
Best Local Similarity
  Conservative
                       100.0%;
  0;
Score 1439; DB 20;
Pred. No. 5.1e-138;
); Mismatches 0;
  Indels
                                         Length 267;
  0;
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Gaps
0;
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Result No.

Score

Match

Length

DB

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Description

SUMMARIES

Query

1439 1340 1340 1340 1333 272.5 266.5

100.0 93.1 93.1 92.6 18.9 18.5

267 349 349 248 214 259

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US-09-654-652A-2 US-09-654-652A-3 US-09-791-537-30441 US-09-654-652A-1 US-09-791-537-145019 US-09-791-537-106873

Sequence Sequence Sequence Sequence Sequence Sequence

2, Appli 3, Appli 30441, A 1, Appli 145019, 106873,

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Sequence 3, Application US/09654652A

GENERAL INFORMATION:
APPLICANT: STYUR, LIE-FEN
APPLICANT: CHEN, JUI-LIN
APPLICANT: YANG, NING-SUM
TITLE OF INVENTION: A TRUNCATED FORM OF FIBROBACTER SUCCINOGENES 1, 3-1,
TITLE OF INVENTION: THERMO-TOLERANCE
TITLE OF INVENTION: THERMO-TOLERANCE
FILE REFERENCE: 4910-8
CURRENT APPLICATION NUMBER: US/09/654,652A
CURRENT APPLICATION NUMBER: US/09-05
NUMBER OF SEO ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
ORGANISM: Fibrobacter succinogenes
                                       US-09-791-537-30441 ; Sequence 30441, Application US/09791537 ; GENERAL INFORMATION:
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Best Local Sim
Matches 250;
            APPLICANT: Bionomix, Inc. APPLICANT: Debe, Derek
APPLICANT:
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Pred. No. 1e-127;
0; Mismatches 1;
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; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF ; TITLE OF INVENTION: METHODS OF USE THEREOF ; FILE REFERENCE: 261/210 CURRENT APPLICATION NUMBER: US/09/791,537 : CURRENT FILING DATE: 2001-02-22 : NUMBER OF SEQ ID NOS: 153055 : SOFTMARE: Patentin version 3.0 : SEQ ID NO 30441 : LENGTH: 349 : TYPE: PAT : ORGANISM: Fibrobacter succinogenes US-09-791-537-30441
                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09654652A
GENERAL INFORMATION:
APPLICANT: SHYUR, LIE-FEN
APPLICANT: SHYUR, JUI-LIN
APPLICANT: CHEN, JUI-LIN
APPLICANT: YANG, NING-SUN
TITLE OF INVENTION: A TRUNCATED FORM OF FIBROBACTER SUCCINOGENES 1, ITTLE OF INVENTION: A TRUNCATED FORM OF FIBROBACTER SUCCINOGENES 1, ITTLE OF INVENTION: THERMO-TOLERANCE
TITLE OF INVENTION: THERMO-TOLERANCE
FILE REFERENCE: 4910-8
CURRENT APPLICATION NUMBER: US/09/654,652A
CURRENT FILING DATE: 2000-09-05
UNMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
LENGTH: 248
TYPE: PRT
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                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Modified ; OTHER INFORMATION: with enhanced activity and thermal stability US-09-654-652A-1
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                VLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVR 120
                                                                              MVSAKDESGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIE
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VLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVR
                                                                  MVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIE
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                                                                                                                                                 92.6%; Score 1333; DB 20; 100.0%; Pred. No. 3.2e-127;
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Pred. No. 1e-127;
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SEQ ID NO 145019
LENGTH: 214
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Best Local :
                                                  SOFTWARE: PatentIn version 3.0 SEQ ID NO 106873
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                                                                                 APPLICANT: Debe, Derek
APPLICANT: Denzer, Joseph
TITLE OF INVENTION: THEE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FILLING DATE: 2001-02-22
RUMBER OF SEQ ID NOS: 153055
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                 APPLICANT: Bionomix, Inc.
TYPE: PRT ORGANISM:
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                                   LENGTH: 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TKVQFNYYTNGVGGH---EKVISLGFDASKGFHTYAFDWQPGYIKWYVDG-VLKHT---A 110
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 Brevibacillus brevis
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US-09-791-537-32335; Application US/09791537
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LENGTH: 252
TYPE: PRT
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SEQ ID NO 1
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Best Local Similarity 35.8%;
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                                            CURRENT APPLICATION NUMBER: US/09/463,862A
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: DE 197 32 751.6
PRIOR FILING DATE: 1997-07-30
PRIOR FILING DATE: 1998-07-21
PRIOR FILING DATE: 1998-07-21
NUMBER: OF SEQ ID NOS: 2
                                                                                                                                                                                                                         APPLICANT: Hillen, Wolfgang
APPLICANT: Maurer, Karl-Heinz
TITLE OF INVENTION: New Beta-Glucanase from
FILE REFERENCE: H2081PCT/US
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEO ID NOS: 153055
SOFTWARE: Patentin version 3.0
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                          SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 SARNYKAGELRTNDFYHYGLFEVSMKPAKVEGTVSSFFTY-TGEWDWDGDPWDEIDIEFL 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKDTTRIQFNYFTNGVGG---NEFYYDLGFDASESFNTYAFEWREDSITWYVNGEAVHTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---TENIPQTPQKIMMNLWPGVGVDGWTGVFDGDNTPVYSYYDWV--
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APPLICANT: Bohomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 6910
LENGTH: 208
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S-09-791-537-6910
Sequence 6910, Application US/09791537
GENERAL INFORMATION:
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                                                                                                                                                                    US-09-791-537-132244
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                                                                                                                          Sequence 132244, Application US/09791537 GENERAL INFORMATION:
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          APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
FILE REFERENCE: 261/210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                                                                                                                                                                                                                                                                                                                                              VSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGSDFTL 184
:|: | | : | ||: || ||
                                                                                                                                                                                                                                                       -WEPK-SYFNPSTWEKADGYSNGGVFNCTWRANNVNFTNDGKLKLGLT
                                                                                                                                                                                                                                                                                              DWTDNFDTFDGSRWGKGDWTFDGNRVDLT--DKNI-YSRDGMLILALT 229
                                                                                                                                                                                                                                                                                                                                        TANIPSTPGKIMMNLWNGTGVDDWLGSYNGAN-PLYAEYDWV---KYT----SNGSVF--
                                                                                                                                                                                                                                                                                                                                                                                                                       TKVQFNYYTNGVGGH----EKVISLGFDASKGFHTYAFDWQPGYIKWYVDG-VLKHT---A 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTRVQFNYFTNGVG----NNEHYHELGFDASESFNTYAFEWRPESISWYVNGELVYTA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EYKAGELRTNQFYQYGLFEVNMKPAKSTGTVSSLFTY-TGPWDWDNDPWDEIDIEFLGKD 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGP---AHGTQWDEIDIEFLGKDT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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36.5%;
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Pred. No. 4.4e-17;
2; Mismatches 73; Indels 13;
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US-09-791-537-117361
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US-09-791-537-117361
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US-09-791-537-132244
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Matches
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 117361
LENGTH: 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Blonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-02-7
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 132244
LENGTH: 394
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Best Local Similarity
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                                    211 DLT--DKNI-YSRDGMLILALTRKGQESFN 237
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                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                             FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                                                      SYNGAN-PLYAEYDWV---KYTSNQ-TGGSFF---
                                                                                                                                                DASKGFHTYAFDWQPGYIKWYVDG-VLKHT---ATANIPSTPGKIMMNLWNGTGVDDWLG
                                                                                                                                                                     AADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVG 150
                                                                                                                                                                                                                      TGIVSSFFTYTGP---AHGTQWDEIDIEFLGKDTTKVQFNYYTNGVGGH---EKVISLGF 55
                                                                                                                                                                                                                                                         SGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSP 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIVNAVNGSGGNYSVNWSNTGNFVVGKGWTTGSPFRTINYNAGVWAPNGN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-----EGGSDFTLDWTDNFDTFDGSRWGKGD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGP---AHGTQWDEIDIEFLGKDT
 NCTWRANNVNFTNDGKLKLGLTSSAYNKFD
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                                                                                                                                                                                                                                                                                                          17.2%; Score 247.5; DB 2 32.9%; Pred. No. 2.8e-16;
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191
                                                                        - EPFNSYNSGTWEKADGYSNGGVF
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RESULT 12

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; TYPE: PRT
; ORGANISM: Bacillus sp
US-09-791-537-31771
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Matches
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SEQ ID NO 27063
LENCTH: 242
TYPE: PRT
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION UMBER: US/09/791,537
CURRENT APPLICATION UMBER: US/09-222
NUMBER OF SEQ ID NOS: 153055
NUMBER OF SEQ ID NOS: 153055
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBI
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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196 ATNQIPTTPGK--IMMNLWNGTGVDEWLGSYNGVN-PLYAHYDWVRYTK 241
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                                                                                                                                                                                                   ω
                                     EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                                                            GKDTTKVQFNYYTNGAG----NHEKIVDLGFDAANAYHTYAFDWQPNSIKWYVDGQ-LKHT
                                                                                                                  GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                     SYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPT---DGTPWDEIDIEFL 139
                                                                                                                                                                                             SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKIQFNYFTNGVGG----NEHYHELGFDAADDFNTYAFEWRPESIRWFVNGELVHTA----
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                                                                                                                                                                                                                                         1 Similarity
60; Conserv
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36.1%;
                                                                                                                                                                                                                                      17.1%; Score 246.5; 35.5%; Pred. No. 4.20 tive 24; Mismatches
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Pred. No. 4e-16;
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4.2e-16;
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Watches 59; Conserve
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US-09-791-537-79889
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Watches 59; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT; ORGANISM: Bacillus subtilis US-09-791-537-73450
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US-09-791-537-73450
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.0 SEQ ID NO 79889 LENGTH: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0 SEQ ID NO 73450 LENGTH: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 73450, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 79889, Application US/09791537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEO ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
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APPLICANT: Debe, Derek
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 261/210
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                                                                              144 TKVQFNYYTNGAG---
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200 IPTTPGK--IMMNLWNGTGVDEWLGSYNGVN-PLYAHYDWVRYTK 241
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                                   VSNLTGTQGLRENLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                                                                                                  GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                         FDCGENRSVQTYGYGLTEVRMKPAKNTGIVSSFFTYTGPT---DGTPWDEIDIEFLGKDT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKVQFNYYTNGAG----NHEKIVDLGFDAANAYHTYAFDWQPNSIKWYVDGQ-LKHTATNQ
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35.8%;
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Search completed: January 9, 2003, 12:13:28 Job time: 127.774 secs

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Result
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1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_nnerreb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel:
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sp_rodent:*
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2312.009 Million cell updates/sec
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Compugen Ltd.
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                            09k7x5 bacillus ha
09apd8 bacillus ci
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045648 bacillus sp
093ge8 uncultured
093ge7 uncultured
093g10 ruminococcu
093ge6 uncultured
045691 bacillus su
08rmp0 bacillus su
08rmp0 bacillus su
09fdc9 paenibacill
07fd3 clostridium
09fd3 clostridium
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         Q8u8n5 agrobacteri
Q98c78 rhizobium 1
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Q9zv40 arabidopsis	Q9ZV40	10	305	7.9	145	ັດ
Q949i0 festuca pra	Q949I0	10	280	7.9	145	4
Q9xij7 arabidopsis	Q9XIJ7	10	310	8.0	145.5	ω
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Q38857 arabidopsis	Q38857	10	284		146.5	ï
P93669 hordeum vul	P93669	10	289		149	Ö
_	Q93UI2	Ν	163	•	153	9
0	Q9SEB0	10	284		154.5	8
Q38907 arabidopsis	Q38907	10	277		154.5	37
Q8xnf8 clostridium	Q8XNF8	16	845		155	6
Q9kwf3 clostridium	Q9KWF3	N	845	8.5	155	5
-	Q9ZRV1	10	292		156	4
Q39148 arabidopsis	Q39148	10	269		157.5	ω
Q9p420 trichoderma	Q9P420	w	94		157.5	Ñ
	Q9HGU1	w	92		157.5	1
0	Q51333	Ν	306	8.7	159.5	õ
Q9zsu4 arabidopsis	Q9ZSU4	10	287		159.5	9
	Q8W4M6	10	286	8.8	160	8
	Q9FKL8	10	284	•	161	7
	Q38910	10	286		164	õ
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$\sim$	Q9M0D2		282	•	170.5	4
Q60039 thermotoga	Q60039		646		171	ũ
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Q9wxn1 thermotoga	Q9WXN1	16	642	•	173	ŭ
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Q9fi31 arabidopsis	Q9F131	10	282	10.1	185	œ
Q9k7x6 bacillus ha	Q9K7X6	16	302	10.4	190.5	.7

## ALIGNMENTS

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                                    Query Match
Best Local Similarity
   Matches
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0987X5; PRELIMINARY;

01-OCT-2000 (TrEMBL:el. 15, Lt

01-DEC-2001 (TrEMBL:el. 19, Lt

Endo-beta-1,3-1,4 glucanase (
                                                                                                                                     EMBL; AP001518; BAB06951.1; -.
HSSP; P23904; 1AJK.
InterPro; IPR000757; Glyco_hydro_16.
InterPro; IPR001899; Gram_pos_anchor.
Ifam; PF00722; Glyco_hydro_16; 3.
Pfam; PF007746; Gram_pos_anchor; 1.
PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSVL_HYDROL_F16; 3.
Hydrolase; Glycosidase; Complete proteome.
SEQUENCE 851 AA; 98142 MW; C1C4F0F158400285 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINB-20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R.
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus halodurans.
Bacillus/Clostridium group; Bacillales;
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   83;
   Conservative
                                 14.7%;
32;
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Last annotation update)
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                                 Score 268.5; DB 1
Pred. No. 7.2e-10;
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   Mismatches
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21 LTTNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEV 80

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Best Local
                                                                    045648 PRELIMINARY:
045648;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee D. -S., Kim J.-Y., Kim H.-B.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ database:
EMBL; AF306531; AAG53947.1; -.
HSSP; P23904; 1AJK.
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRAAE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
SEQUENCE 256 AA; 27604 MW; 989E50C09F6E4531 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9APD8;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Endo-beta-1,3-1,4-glucanase.
                                              Lichenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-ATCC21367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9APD8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNCSGKPYASAEYATTQKYGYGRVEARIKAAKGTGLVTSLFTY---SGAAPGTSNDEIDI 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVH-TETGSRGPLPTSPGYIMVNLWSGAGPAEIWTGKFTYPGHPIRAYYDWI---KFTP
                                                                                                                                                                                                                                                                                                                                                                      EVRKTEGGQVSNLTGTQG-LRFNLWSSESAA--WVGQFDESKLPLFQFINWVKVYKYTP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QMFNATWYDSQITFSNGIMRFAIDKE------DDEEA 351
                                                                                                                                                                                                                                                                                                                                                                                                                             EILGKDTTKMETNYFTNGVGGHST-----VIDLGFDASLDFHDYAFEWSPTSIKWYVDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQA--FHTYGLEWTPNYVRWTVDGQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRVDLT--DKNIYSRDGMLILALTRKGQESFNGQVPRDDEPA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALDEEESGDDNEEEPVEEVEEEPAEDEEVSVRPIGSAIYETFNTFNEDIWSIAHGWT-NG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIEFLGKDTTRIQFNYFTNGVGG---NEFYYDLGFDASESFNTYAFEWREDSITWYVNGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                 precursor
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Last sequence update)
Last annotation update)
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Pred. No. 1.3e-09;
                                                                                                                                                                                      PRT;
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Best Local
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Best Local Similarity
Matches 61; Conserv
                                                                                            Matches
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SIGNAL
                                                                                                                                                           Rodriguez V., Mellado R.P.;
"Novel lichenases from soil.";
"Novel lichenases from soil.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF254957; AAK50610.2; -.
InterPro; IPR007757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PROSTIE; PS01034; GLYCOSYL_HYDROL_F16; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                               Q93GE8
Q93GE8; PRELIMINARY;
Q1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                       Endo 1-3,1-4-beta-glucanase uncultured bacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and DNA sequencing of bgaA, a gene encoding 1, 4-glucanase, from an alkalophilic Bacillus strain Appl. Environ. Microbiol. 60:1213-1220(1994).
EMBL; 212151; CAA/8135.1; -.
HSSP; P23904; 1AJK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94288605; PubMed-7517127;
Tabernero C., Coll P.M., Fernandez-Abalos J.M.,
Santamaria R.I.;
                                                                                                                                                                                                                                                                                             NCBI_TaxID=77133;
                                                                                                                                                                                                                                                                                                          Bacteria; environmental samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Iffam; PF00772; Glyco_hydro_16; 1.
PRINTS; PR00737; GLYCOSYL_HYDROL_F16;
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
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EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 89
                                        TSPSYNKFDCGENRSVQTYGYGPYEVRMKPAKNTGIVSSFFTYTGPTE----GTPWDEIDI 108
                                                              TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSNLTGT-QGLRENLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKIQFNYFTNGVGG----NEHYHELGFDAADDFNTYAFEWRPESIRWFVNGELVHTA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YKAGELRTNDFYHYGLFEVSMKPAKSTGTVSSFFTY-TGPWDWENDPWDEIDIEFLGKDT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TENIPQTPQKIMMNLWPGIGVDGWTGRFNGEDTPVVTQYDWV----KYTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ
                                                                                                        Similarity
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32
276 AA;
                                                                                                                                               214 AA;
                                                                                           Conservative
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276 L
31770 MW;
                                                                                                                                               24159 MW; 3DB186D3B9D991CF CRC64;
                                                                                                      13.5%;
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Last annotation update
                                                                                         Score 246.5; DB 2
Pred. No. 3.6e-09;
5; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 247.5;
Pred. No. 4.3
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; D047F8A34CA9EBE2 CRC64;
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                                                                                                                   DB 2;
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                                                                                                                  Length
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(N137).";
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Qy dy

143

EFLGKDTTKVQFNYYTNGAG---NHEKLADLGFDAANAYHTYAFDWQPNSIKWYVDGQ-L RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 193

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109

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RESULT
Q9S310
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Best Local :
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Bacteria; environment
                                                                                                                                                                                                                                                                                                                                                                                                           Q9S310 PRELIMINAKI,
Q9S310;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
O1-JUN-2002 (TremBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium Clostridiales; Lachnospiraceae; Ruminoco-NCBI_TaxID=1265; [1]
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Q93GE7;
01-DEC-2001
01-DEC-2001
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"Novel lichenases from soil.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ
EMBL; AF254959; AAK50612.2;
EMBL; AF254959; AAK50612.2;
InterPro; IPR000757; Glyco.hydro_16.
Pfam; PF00722; Glyco.hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
                                              Submitted (FEB-1999) to the EMBL; AJ132472; CAB51934.1; HSSP; P23904; IAJK.
                                                                                                                          Aurilia V., Martin J.C., Munro C.A., Mercer D.K., Flint H.J., "Organisation and strain distribution of genes responsible foutilization of xylans by the rumen cellulolytic bacterium Rum flavefaciens 17.";
                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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NCBI_TaxID=77133;
                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KHTATTQIPAAPGK--IMMNLWNGTGVDDWLGSYNGVN-PLYAHYDWVRYTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
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IPR003305; CBM_CenC IPR001137; GH_11.
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                                                                                                                                                                                                                                                                                                                                  Lachnospiraceae; Ruminococcus
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Pred. No. 4.
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                                                                                                                                                       Ruminococcus
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IJ

Q45691

PRELIMINARY;

PRT;

239

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R Pfam; PF02018; CBM_4_9; 2.

R Pfam; PF02018; CBM_4_9; 2.

JR Pfam; PF00457; Glyco_hydro_11; 2.

Pfam; PF00722; Glyco_hydro_16; 2.

DR PRINTS; PR00737; GLHYDRLASE11.

DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 2.

DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 2.

DR PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 2.

PAMILY 16; 7:3-1,4) GLUCANASE /FAMILY 16; 7:3-1,4) GLUCANASE.
RESULT 8
Q45691
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Best Local
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Rodriguez V., Mellaud n....
"Novel lichenases from soil.";
"Submitted (SEP-2001) to the EMBL/GenBank/DDBJ
EMBL; AF254961; AX350614.2; -.
InterPro; IPR000757; Glyco_hydro_16.
Dfam: PF00722; Glyco_hydro_16: 1.
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Q93GE6;
Q1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endo 1-3,1-4-beta-glucanase
uncultured bacterium.
                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria;
                                                                                                                                                                                                                                                                                                           PROSITE; PS01034; GLYCÓSYL_HYDROL_F16; UNKNOWN_1.
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                                                                                                                                                                           TSPSYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDI 108
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                                                       KHTATTQVPAAPGK--IMMNLWNGTGVDDWLGSYNGVN-PLYAHYDWVRYTK
                                                                                    RKTEGGQVSNLTGTQGLRENLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 193
                                                                                                               ESLGKDTTKVQFNYYTNGAG----NHEKLADLGFDAANAYHMYAFDWQPNSIKWYVDGQ-L
                                                                                                                                              EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
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Pred. No. 1.1
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Best Local
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Q1-JUN-2002 (TrEMBLrel.
Q1-JUN-2002 (TrEMBLrel.
Q1-JUN-2002 (TrEMBLrel.
Beta-1,3-1,4-glucanase.
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01-NOV-1996
01-NOV-1996
01-DEC-2001
Endo-beta-1;
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"Over-expression of the Saccharomyces cerevisiae exo-beta-1,3-
glucanase gene together with the Butyrivibrio fibrisolvens endo-beta-
1,4-glucanase gene and the Bacillus subtilis endo-beta-1,3-1,4-
glucanase gene in Saccharomyces cerevisiae.";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U60830; AAB05759.1;
EMBL; D60830; AAB05759.1;
                                                                                                                                                                                                                                                      Sun J., Li W., Gu S., Xu Z., Zhao H., Xiao J.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ
EMBL; AF490978; AAM08358.1; -.
SEQUENCE 242 AA; 27238 MW; 285FED3FE76AE69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00722; Glyco_hydro_16; 1.

PRINTS; PR00737; GLHYDRLASE16.

PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.

SEQUENCE 239 AA; 26969 MW; C4219760D13F878A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8RMP0
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NCBI_TaxID=1423;
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Bacteria; Firmicutes;
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                                                                                                                                                                                          Local
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                                                                                                                                                                                                               Match
                                                                                              TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI 82
EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV
                                                                   TSPSYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPT---DGTPWDEIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q-LKHTATTQIPTAPGK--IMMNLWNGTGVSDWLGSYNGVN-PLYAHYDWVRYTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QEVRKTEGGQVSNLTGTQGLRFNLWSSESAA-WVGQFDESKLPLFQFINWVKVYK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPA---ADQAFHTYGLEWTPNYVRWTVDG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSPSYNKEDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
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                                                                                                                                                                 Conservative
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Pred. No. 1.
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                                                                                                                                                                                                                                                        285FED3FE76AE69A CRC64;
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Best Local
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Q9FDC9;
01-MAR-2001
01-MAR-2001
                                                                                                                                                                           OO7856 PRELIMINARY; PRT;
OO7856;
O1-JUL-1997 (TrEMBLrel. 04, Created
O1-JUL-1997 (TrEMBLrel. 04, Last se
O1-DEC-2001 (TrEMBLrel. 19, Last an
Beta-(1,3-1,4)-glucanase precursor.
        beta-(1,3-1,4)-glucanase fro
Submitted (MAR-1997) to the
EMBL; Z92911; CAB07443.1; -.
                                                             STRAIN-JB1;
Ekinci M., Flint H.J.;
                                                                                                              Streptococcaceae;
NCBI_TaxID=1315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01034; GLYCOSYL_HYDROL_F16; NON_TER 1 1 1 1 NON_TER 212 212 SEQUENCE 212 AA; 24127 MW; 7E707E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000757; Glyco_hydro_16
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Yao W., Wang Y., Song W., Yang K., Su Z.;
"Gene cloning of an antifugal protein.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ
EMBL; AF284449; AAG02415.1;
HSSP; P23904; 1AJK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endo-1,3-1,4-beta-glucanase (Fragment).
Paenibacillus polymyxa (Bacillus polymyxa).
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Paenibacillaceae; Paenibacillus.
                                  "Isolation and overexpression of a gene encoding an extracellular beta-(1,3-1,4)-glucanase from Streptococcus bovis JBL.";
                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                       Streptococcus bovis.
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                                                                                        SEQUENCE FROM
                                                                                                                                                                      LICHENASE
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                                                                                                                                                                                                                                                                                                                                        QEVRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT
                                                                                                                                                                                                                                                                                                                                                                                           VDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDG
                                                                                                                                                                                                                                                                                                                                                                                                                    SLTSSAYNK-FDGGEYRSKNTYRYGLYEVNMKPAKNTGIVSSFFTYTGP---ANGTQWDE 103
                                                                                                                                                                                                                                                                                                               -VLKHT---ATTNIPKTPGQIMMNLWNGTGVDSWLGPYNGVN-PLYAEYDWV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KHTATNQIPTTPGK---IMMNLWNGTGVDERLGSYNGVN-PLYAHYDWVRYTK
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                                                                                                                                                                                                                                                                                                                                                                   IDIEFLGKDTTKVQFNYYTNGIGGH----EKVVDLGFDASSGFHTYAFDWQPGYIKWYVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFLGKDTTKVQFNYYTNGAG----NHEKIVDLGFDAANAYHTYAFDWQPNSIKWYVDGQ-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
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                                                                                       N.A.
                                                                                                                             Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
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Last annotation updat
                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                        Created)
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Pred. No. 3.1
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                                                                                                                                          Lactobacillales;
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Q93UIT 12
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Best Local S
Matches 56
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Q93UI1;
01-DEC-2001
01-DEC-2001
  Q97FD3;
Q97FD3;
Q1-OCT-2001
Q1-OCT-2001
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Novel lichenases from soil.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF254960; AAK50613.1; .
Interpro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rodriguez V., Mellado R.P.;
                                                                                                                                                                                                                      165
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                                                                                                                                                                                                                                                                                                                             109
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                                                                                                                                                                                                                   KHTATTQVPAAPGK -- IMMNLWNGTGVDDWLGSYN 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSNLTGTQG-LRENLW--SSESAAWVGQFDESKLPLFQFINWV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 149
                                                                                                                                                                                                                                                                     RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                 TSPSYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YNNIPSTPGKIMMNAWPGTHEVDSWLGAYN-GRTPLYAYYDWI
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                                                                                                                                                                                                                                                                                                                       ESLGKDTTKVQFNYYTNGAG----NHEKLADLGFDAANAYHMYAFDWQPNSIKWYVDGQ-L
                                                                                                                                                                                                                                                                                                                                                                         EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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  (TrEMBLrel. (TrEMBLrel.
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                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.2%; Score 223; DB 2; 36.1%; Pred. No. 1.3e-07; tive 21; Mismatches 68
18,
18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26; Mismatches
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Last annotation updat
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Pred. No. 5.
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BETA-(1,3-1,4)-GLUCANASE.
, 7DEF5BCE53790470 CRC64;
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                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E7CADAAFE02A2F51 CRC64;
                                                                                   246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 205;
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RESULT 14
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Best Local S
Matches 58
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Q1-JUN-2002 (TremBirel. 21, Crea
Q1-JUN-2002 (TremBirel. 21, Last
Q1-JUN-2002 (TremBirel. 21, Last
Endo-1,3-1,4-beta-glycanase.
EXOK OR ATU4055 OR AGR_L_1600.
                                                                                                                                                                   SEQUENCE FROM N.A.

MEDIINE-21608550; PubMed-11743193;

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo I

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo I

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin T., Levy R., Saenphimmachak C., Wu Z., Romero P., Gordo

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordo

Thomas C., Wood G., Saenphimmachak C., Wu Z., Romero P., Gordo
                        "The genome of the natural genetic engineer Agrobacterium tumefaciens {\tt C58."};
                                                                                               Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agrobacterium tumefaciens (strain C58 / ATCC Bacteria, Proteobacteria; alpha subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8U8N5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium Clostridiales; Clostridiaceae; Clostridium
Science
                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00722; Glycc_hydro_16
PRINTS; PR00737; GLHYDRLASE16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacterium Clostridium acetobutylicum.
J. Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-ATCC
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                                                                              Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000757; Glyco_hydro_16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE007778; AAK80751.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 ---TSNIPTHPGKVMMNLWPGIGVDSWLGAYD-GVTPVKAYYNWA---MYNP 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGQVSNLTGTQG-LRENLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP 196
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58; Conser
294:2317-2323(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobium.
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33.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
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.2e-07;
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Rhizobiaceae
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                                                                                                                             Perry M.,
Dolan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      group;
                                                                                                                                                                                   Gordon D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
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Best Local S
Matches 51
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                                                                                                                                                                                                                                  "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
DNA Res. 7:331-336(2000).
EMBL; AP003006; BABS1743.1; -
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRIASE16.
Complete proteome.
SEQUENCE 293 AA; 32347 MW; 93BBA1672176ED3C CRC64;
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MEDLINE-2160851; PubMed-11743194;
GOODINE B., Hinkle G., Gattung S., Miller N., Blanchard M.,
GOODINE B., Hinkle G., Gattung S., Miller N., Halling C., Mullin L.,
Ourollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
"Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
Science 294:3237-3238 (2001).
EMBL; AE009336; AAL44856.1; ALT_INIT.
EMBL; AE009379; AAK89373.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamot Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M. Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
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112 REFACGEIQTKORFGYGTYEARLKTDTGSGLNAAFFTYIGPS---DKQPWDEIDFEILTK 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNFACGEIQTKGRYRYGTYEARMKAATGSGLNSAFFTYIGPT---DKKPHDEIDFEVLGK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l,3-1,4-beta-glycanase,
                                                                                                                    Similarity 33.8
51; Conservative
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Proteobacteria; alpha subdivision; Rhizobiaceae group;
teriaceae; Mesorhizobium.
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                                                                                                                 11.0%; Score 200; DB 1
33.8%; Pred. No. 7e-06;
tive 27; Mismatches
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Last annotation update)
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                                                                                                                                                                             DB 16; Length 293;
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imura T.,
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Search completed: January 9, 2003, 12:18:13 Job time: 32.103 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Endo-1,3-1,4-beta-glycanase exoK precursor (EC 3.2.1.-) (Succinoglycan
                                                                                                                               Gosalbes M.J., Perez-Gonzalez J.A., Gonzalez R., Navarro A.;
"Two beta-glycanase genes are clustered in Bacillus polymyxa:
molecular cloning, expression, and sequence analysis of genes
encoding a xylanase and an endo-beta-(1,3)-(1,4)-glucanase.";
J. Bacteriol. 173:7705-7710(1991).
-:- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages
in beta-D-glucans containing 1,3- and 1,4-bonds.
-:- MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANGE
SIMILAR TO LICHENASE OF GERMINATING BARLEY.
-:- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 VDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 IDIEFLGKDTTKVQFNYYTNGVGGH---EKIINLGFDASTSFHTYAFDWQPGYIKWYVDG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 ALTINVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVE 79
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase) (1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase) GLUB.
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                                                  Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus NCBI_TaxID=1406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae grou
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NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
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EXOK OR RB1080 OR SMB20955.
Rhizobium meliloti (Sinorhizobium meliloti).
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                                              Paenibacillus polymyxa (Bacillus polymyxa)
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PRIMTS: PR00722; Glyco_hydro_16; 1.
PRIMTS: PR00737; GLHYDRLABEL6.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
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                                                                                                                        MEDLINE=92041687; PubMed=1938968;
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                                                                                                SEQUENCE FROM N.A.
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 RKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINMVKVYKYT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 237;
                                                                                                                                               NUCLEOPHILE (BY SIMILARITY). PROTON DONOR (BY SIMILARITY).
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; Pred. No. 1.5e-09;
25; Mismatches 74
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Last sequence update)
Last annotation update)
                                                          PEDS, TOTAL PRODUCTO, STATE OF THE PROPERTY OF THE PRINTS; PRODUCTO, GLYCOLNGROLES, 1. PROSTE; PRO1034; GLYCOSYLLHYDROLETE; 1. PROSTE; PSGIOSSE, GLYCOSYLLHYDROLETE; 1. 23 POTENTIAL.
                                                                                                                                      BETA-GLUCANASE.
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Best Local Similarity 34.35
Matches 60; Conservative
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                        27-FEB-95.
06-MAY-98.
06-MAY-98.
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225 2
237 AA;
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Exopolysaccharide synthesis; Glycosidase; Hydrolase; Signal; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                       Becker A., Kleickmann A., Arnold W., Puehler A., "Analysis of the Rhizobium meliloti exoH/exoK/exoL fragment: ExoK shows homology to excreted endo-beta-1,3-1,4-glucanases and ExoH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
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ACGEIQTRKR -> LRRNPDAQG (IN REF.
073CC7ED65EF2611 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             York G.M., Walker G.C., "The Rhizobium meliloti ExoK and ExsH glycanases specifically
                                                                                                                                                                        Glucksmann M.A., Reuber T.L., Walker G.C.;
"Family of glycosyl transferates needed for the synthesis of succinoglycan by Rhizobium meliloti.";
J. Bacteriol. 175:7033-7044(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.8%; Score 197; DB 1; Length 269; llarity 32.5%; Pred. No. 2.8e-07; Conservative 31; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY: Exopolysaccharide biosynthesis. SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
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HSSP; P23904; LAJK.
INTELPIO; IPRO00757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              resembles membrane proteins.";
Mol. Gen. Genet. 238:145-154(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-1021;
MEDLINE-21396508; PubMed-11481431;
                                                                                                                                                                                                                                                                                                                                             STRAIN-RCR2011 / SU47;
MEDLINE-93241147; PubMed-8479421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98226741; PubMed-9560202;
                                                                                                                                          MEDLINE-94042869; PubMed-8226645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 A
30083 MW;
   Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L20758; AAA16048.1; -.
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                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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50;
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                    85 LGKNPGSFQSN-IITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVR 143
                                                                                               "The gene clusters ARC and COR on chromosomes 5 and 10, respectively,. of Saccharomyces cerevisiae share a common ancestry.";
J. Mol. Biol. 233:372-388(1993).
-!- SIMILARITY: SOME, TO YEAST YGR189C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-S288C / AB972;
Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzall G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
   84
25 VSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEV
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Multiple F.S., Hennessey K.M., Sehl P., Komp Mulligan J.T., Dietrich F.S., Hennessey K.M., Sehl P., Komp Wei Y., Taylor P., Nakahara K., Roberts D., Davis R.W.; Submitted (FEB-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetales; Saccharomycetaceae; Saccharomyces
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                            (Rel. 27, Created)
(Rel. 30, Last sequence update)
(Rel. 34, Last annotation update)
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POLY-SER.
L -> V (IN REF. 3
A -> R (IN REF. 3
                                                                                                                                                                                                                                                                                                                                                                      UTR2 protein (Unknown transcript 2 protein).
UTR2 OR YEL040W OR SYGP-ORF18.
                                                                                                                                              144 K-TEGGOVSNLTGTQGLRFNLWSSESAA-WVGQF 175
                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000757; Glyco_hydro_16.
                                                                                                                                                                                                                                                                              PRT;
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EMBL; L22173; AAA141.1; -.
EMBL; S65564; AAD13975.1; -.
EMBL; S66130; AAB28444.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=B-6441;
MEDLINE=94016558; PubMed=8411151;
Melnick L., Sherman F.;
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322 SE
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171
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SGD; S0000766; UTR2.
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                                                                                                                                                                                                                                                                                                                01-OCT-1993
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01-OCT-1996
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 AQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRF- 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spilliaert R., Hreggvidsson G.O., Kristjansson J.K., Eggertsson G., Palsdottir A.; "Cloning and sequencing of a Rhodothermus marinus gene, bglA, coding for a thermostable beta-glucanase and its expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        TAVKSALAVAAAAAALTTNVS----AKDFSGAELYTLE------EVQYGKFE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 TLLVAAFSVSAADFNTDVNVAWGNGRGKILNNGQLLTLSLDKSSGSGFQSKTEYLFGKID 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
(1,3-1,4-beta-D-glucan 4-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: SHOWS ACTIVITY ON LICHENAN, BETA-GLUCAN AND LAMINARIN BUT NOT ON CMC CELLULOSE OR XYLAN. THE ENZYME HAS A TEMPERATURE
                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhodothermus marinus (Rhodothermus obamensis).
Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;
Crenotrichaceae; Rhodothermus.
                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 269;
                                                                                                                                                                                                                                                                                                                                                                8.6%; Score 157.5; DB 1; Length 25.2%; Pred. No. 0.00019; Live 39; Mismatches 76; Indels
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GS -> DR (IN REF. 7).
A -> G (IN REF. 1).
G48F042BC7ADED86 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 KNKPMRMYASLWNADDWATRGGLVKTDWSKAPFMASYRNIKI 217
                                                                                            286 AA
                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                    EMBL; M63166; AAA32828.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem. 224:923-930(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-21 / ITI-378;
MEDLINE-95010084; PubMed-7925416;
                                                                                                                                                                                                                                                                                                                                      30755 MW;
                                                                                                                                                                                                                                                                                                                                                                               1 Similarity 25.2 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                            269
94
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93
184
169 AA;
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P45798;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -EVLGKNP----GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGQEVRKTEGGQVSNLTG-----TQGLRFNLWSSESAAWVGQ--FDESKLPLFQFINW 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDSLYYRFPNERLTDPEADWRHWPFDQPFHLIMNIAVGGAWGGQQGVDPEAFPAQLVVDY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene from elongating soybean (Glycine max L.) epicotyls.";
Plant Physiol. 104:161-170(1994).
-!- FUNCTION: POSSIBLE ROLE IN BRASSINOSTEROID-STIMULATED ELONGATION.
             CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds. SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 KDFSGAELYTLEEVQ--YGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWV---EVDI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycine max (Soybean).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosida eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 286;
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                                                                                                                                                                                                                                                                                                                                                                 BETA-GLUCANASE.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
7215C33624135191 CRC64;
OPTIMUM OF 85 DEGREES CELSIUS AND A PH OPTIMUM OF 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85;
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15-JUN-2002 (Rel. 41, Last annotation update)
Brassinosteroid-regulated protein BRU1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 0.01; 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.3%; Score 133.5; 23.7%; Pred. No. 0.0
                                                                                                                                                                                                                                                                 InterPro; IPR000757; Glyco_hydro_16.
Pfam: PF00722; Glyco_hydro_16; 1.
ProSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
Hydrolase; Glycosidase; Signal.
SIGNAL 1 30 POTENTIAL.
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MEDLINE=94159788; PubMed=8115544;
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                                                                                                                                                                                                                                                                                                                                                                                                                         33145 MW;
                                                                                                                                                                                                                                                 EMBL; U04836; AAA60459.1; -
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158
163
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158 1
163 1
286 AA;
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ACT_SITE
SEQUENCE
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MEDLINE-20083488; PubMed-10617198;
MAPER K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller Kreis M.,
Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
                                                                                                                                                 S DIETAQTNEYWESVLNYTNSANISTTD-----TFENYHTYELDWHEDYVTWSIDGY 105
                                                                                                                                                                                                                                                                                 287
                                                                                                                                  88 NPGSFQSNI-----ITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQ 140
                                                                                                                                                                                141 EVRKTEGGQVSNLTGTQGLRF----NLW---SSESA----AWVG---QFDESKLP 181
                                                                                                                                                                                                       106 VGRTLYKNETYNAT-TQKYQYPQTPSKVDISIWPGGNSTNAPGTIAWSGGEINWDASDIS 164
                                                                                                                                                                                                                                 ----LFQFINWVKVYKYTPGQGEGGSDFTLDWTDNFDTFDGSRWGKGDWTFDGNRVDLTD 237
                                                                                                                                                                                                                                                                                                       213 DEVMMDSDEG-----SGLDPHKGAT----TSSTQKSSSSTATSSSKTSSDHSSSTKK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                             Gaps
                                                                                  28 KDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGK 87
                                                                                                        3 KNSGGTVLSSTRAVWYGKVSARIKTSHLAGVVTGFILYSGAGD------ELDYEFVGA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medford J.I., Elmer J.S., Klee H.J.; "Molecular cloning and characterization of genes expressed in shoot
                                                                                                                                                                                                                                                                                                                                                                                                             MERS_ARATH STANDARD; PRT; 269 AA.
P24806: 039148; Q41904; O64956;
01-MAR-1992 (Rel. 21, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
endo-1,4-beta-D-glucanase).
MERI-5 OR MERISB OR SEN4 OR A74G30270 OR F9N11.120.
                                                                                                                                                                                                                                                       165 NPGYYYAIVNEVNITCYDP----PSDTKKNGTSAYVYTSSSE-----FLAKDIAITD
                                                                                                                                                                                                                                                                               KNIY--SRDGMLILALTRKGQESFNGQVPRDDEPAPQSSSSAPASSSSVPAS-----
                                                            85;
                                    DB 1; Length 347;
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaminal T., Tomita E., Nishitani K.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAILW-cv. Columbia;
Arrowsmith D.A.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
S -> C (IN REF. 3).
1E8AFB862C4BB328 CRC64;
                                                           49; Mismatches 120;
                                   Score 189.5; DB 1
Pred. No. 1.3e-06;
                                                                                                                                                                                                                                                                                                                              ---SSSVPASSSSAFVPPSSSSATNAIHGMRTTPAVA 321
                                                                                                                                                                                                                                                                                                                                             261 SSKTSSTASSSSSSSSSSSTATKNGDKVVSSVS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93005704; PubMed-1840916;
           36692 MW;
                                   10.4%;
24.6%;
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                                                           83; Conservative
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STRAIN=cv. Columbia;
Kamimai T., Tomita E.
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STRAIN-cv. Columbia;
           347 AA;
                                               Similarity
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           SEQUENCE
                                   Query Match
 CONFLICT
                                                 Best Local
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                                                           Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Nos P., Hobelsel J., Zimmerann W., Waeller H., Ridley P., Langham S.-A., McCullagh B., Bilham L., Robban J., Vandenbussche F., Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F., Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F., Walter B., Weltzenegger T., Bothe G., Ramaperger U., Hilbert H., Braun M., Melzer E., Brandt A., Peters S., Van Staveran M., Ditkse W., Mooijman P., Klein Lankhorst R., Nase M., Hauf J., Koetter P., Bernelser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., Bernelser S., Hampel S., Cronin A., Quall M., Bersy Allen S., Ava Mooiragu M., Rogers J., Cronin A., Quall M., Bersy Allen S., And Does S., de Haan M., Marse A.C., Schaefer M., Meltarda K., Mayes R., Bertett A., Rajandream M.A., Lyne M., Benes V., Rechman S., Agabel C., Euchs M., Fartann B., Granderath K., Deunert D., Herzl A., Rabel C., Rabal C., Muendlein A., Felber R., Schmidt W., Ether W., Petrer D., Merzl A., Massenet O., Quigley F., Clabaud G., Muendlein A., Pelber R., Schmidt W., Lecharny A., Aubourg S., And Childer R., Schmidt W., Eartens D., Herzl A., Massenet O., Quigley F., Schmidt W., Earens P., Herline C., Schwarz S., Schwarz S., Schwarz S., Schwarz S., Scholler P., Heber S., Francs P., Bleike C., Raccarla P., Hease D., Lemcke K., Mewes H.-W., Stocker S., Stoneth J., Shedt P., Heber S., Francs P., Bleike C., Scholler P., Heber S., Francs P., Bleike C., Scholler P., Heber S., Francs P., Berlick J., Shedt P., Hobott A., Scholler V., Hunnig E., Splagel L., Scholler P., Heber S., Francs P., Berlick J., Shedt P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., Atterellle P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., Atterellle P., Coutney J., Sheet P., Cordes W., Willer M., Matero A., Scholler W., Marzay S., Scholler W., Marzay S., Scholler W., Marzay S., Scholler W., Watter M., Marzay M., Stonekling T., Kallcki J., Graves T., Hunno G., Edwards J., Fulton L., Scholk M., Stonekling T., Kallck Plant Mol. Biol. 37:445-454(1998).

-!- FUNCTION: Involved in cell wall reconstruction.

-!- TISSUE SPECTRICITY: EXPRESSED IN SHOOT APICAL MERISTEMS, ALSO

-!- SIMILARITY: BELONGS AND MERISTEMS.

-!- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.

-!- CAUTION: Ref. 1 sequence differs from that shown due to frameshifts in positions 158: 178: 189: 189: 190: 194 and 199.

-!- CAUTION: Ref. 6 sequence differs from that shown due to frameshifts in positions 93 and 104. Ξ, STRAIN-cv. Columbia; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the Park J.-H., Oh S.A., Kim Y.H., Woo H.R., Nam H.G.; "Differential expression of senescence-associated mRNAs during leaf STRAIN=cv. Columbia; TISSUE-Green siliques; Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., Delseny M.; Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases. senescence induced by different senescence-inducing factors Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. consortium (Salk/Stanford/PGEC) SEQUENCE OF 1-120 FROM N.A. STRAIN-cv. Columbia; TISSUE-Leaf; MEDLINE-98278374; PubMed-9617812; SEQUENCE OF 1-132 FROM N.A. Nature 402:769-777(1999). SEQUENCE FROM N.A. Arabidopsis." thaliana

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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                         72 ADGRPWVEVDIEVLGK---NPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEW 128
                                                                                                                                                                                                                                                                                                                                                                                                                 129 TPNYVRWTVDGQEVRKTEGGQVSNL--TGTQGLRF--NLWSSESAAWVG---QFDESKLP 181
                                                                                                                                                                                                                                                                                                                     27 AKDFSGAELYTL-------EEVQYGKFEARMKMAA--ASGTVSSMFLYQNGSEI 71
                                                                                                                                                                                                                                                                                                                                             BRASSINOSTEROID-REGULATED PROTEIN BRU1; C248810EC7835737 CRC64;
                                                                                                                                                                                                                                                Query Match 7.0%; Score 128; DB 1; Length 283; Best Local Similarity 23.7%; Pred. No. 0.026; Matches 46; Conservative 41; Mismatches 73; Indels
                                                                EMBL; L22162; AAA81350.1; -.
HSSP; P23904; IAJK.
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF0072; Glyco_hydro_16; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
Glycosidase; Hydrolase; Signal.
SIGNAL 1 30 POTENTIAL.
CHAIN 31 283 BRASSINOSTEROIT SEQUENCE 283 AA; 32254 MW; C248810EC7835
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Search completed: January 9, 2003, 12:16:49 Job time : 9.88657 secs

216 FTAYYRNFKAIEFS 229

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US-09-654-652A-1
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Sequence 2, Appli
Sequence 3, Appli
Sequence 30441, A
Sequence 145019,
Sequence 106873,
                                                                                                                                                                          January 9, 2003, 11:50:42; Search time 115.824 Seconds (without alignments) 1368.672 Million cell updates/sec
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1 MVSAKDFSGAELYTLEEVQY......TRKGQESFNGQVPRDDEPAP
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2: /cgn2_6/ptodata//paa/USO6_COMB.pep:*

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10: /cgn2_6/ptodata//paa/USO9_COMB.pep:*

10: /cgn2_6/ptodata//paa/USO9_COMB.pep:*

11: /cgn2_6/ptodata//paa/USO9_COMB.pep:*

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18: /cgn2_6/ptodata//paa/USO9_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-654-652A-2
US-09-654-652A-3
US-09-791-537-30441
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US-09-791-537-106873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4569144 segs, 644733110 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence:
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18679, A
103817,
67048, A
72848, A
30440, A
88873, A
76270, A
103320,
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US-09-791-537-13171

US-09-791-537-13171

US-09-791-537-13171

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US-09-791-537-10334

US-09-791-537-103817

US-09-791-537-10335

US-09-791-537-103819

US-09-791-537-103819
265.5
257.5
256.5
247.5
247.5
245.5
245.5
245.4
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## ALIGNMENTS

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Sequence 1, Application US/09654652A
GENERAL INCPRAMATION:
APPLICANT: SHUR, JUI-LIN
APPLICANT: CHEN, JUI-LIN
APPLICANT: ANG. NING-SUN
TITLE OF INVENTION: THERMO-TOLERANCE
FILE REPERENCE: 4910-8
CURRENT APPLICATION NUMBER: US/09/654,652A
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 1
LENTH: PART
ORGANISM: Artificial Sequence
FEATURE:
ORGANISM: Artificial Sequence
FEATURE:
ORGANISM: Artificial Sequence
FEATURE:
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Modified enzyme
OTHER INFORMATION: with enhanced activity and thermal stability
US-09-654-652A-1

Query Match
Best Local Similarity 100.0%; Pred. No. 3.4e-130; Indels 0; Gaps 0;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 MVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIE 60

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TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: SHYUR, LIE-FEN
APPLICANT: CHEN, JUI-LIN
APPLICANT: YANG, NING-SUN
TITLE OF INVENTION: A TRUNCATED FORM OF FIBROBACTER SUCCINOGENES 1, 3-1,
TITLE OF INVENTION: THEMA-D-GLUCANASE WITH IMPROVED ENZYMATIC ACTIVITY AND
TITLE OF INVENTION: THEMA-D-GLUCANASE WITH IMPROVED ENZYMATIC ACTIVITY AND
TITLE OF INVENTION: THEMA-COLLERANCE
FILE REFERENCE: 4910-8
CURRENT APPLICATION UNMBER: US/09/654,652A
CURRENT APPLICATION UNMBER: 2000-09-05
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 2
LENGTH: 267
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                                                  KTEGGQVSNLTGTQGLRFNLWSSESAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTEGGQVSNLTGTQGLRFNLWSSESAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 267;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1333; DB 20;
11arity 100.0%; Pred. No. 3.8e-130;
Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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241 PRDDEPAP 248
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US-09-654-652A-2
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US-09-654-652A-3
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ. ID NOS: 153055
SOFTWARE: PAtentin version 3.0
SEQ. ID NO 30441
APPLICANT: CHEN, JULIAN

APPLICANT: CHEN, JULIAN

TITLE OF INVENTION: A TRUNCATED FORM OF FIBROBACTER SUCCINOGENES 1, 3-1,

TITLE OF INVENTION: A "BETA-D-GLUCANASE MITH IMPROVED ENZYMATIC ACTIVITY AND

TITLE OF INVENTION: THERMO-TOLERANCE

FILE REFERENCE: 4910-8

CURRENT APPLICATION NUMBER: US/09/654,652A

CURRENT FILING DATE: 2000-09-05

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PALENTIN Ver. 2.1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 TEGGQVSNLTGTQGLRFNLWSSESAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGSD
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100.0%; Pred. No. 1.9e-129;
Live 0; Mismatches 0;
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100.0%; Pred. No. 1.9e-129;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 247; Conservative
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Best Local Similarity 100.
Matches 247; Conservative
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|RDDEPAP 271
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APPLICANT: Bionomix, Inc.
APPLICANT: Bobbe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Denzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY I
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 32335
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                                                                                                                       3 SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62
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                                                                                                                                                                                                                                                                                             123 EGGQVSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTPGQ 175
                                                                                                                                                                                                                                                                                                                     206 ----TENIPQTPQKIMMNLWPGVGVDGWTGVFDGDNTPVYSYYDWV----RYTPLQ 253
                                           Length 259;
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APPLICANT: Hillen, Wolfgang
APPLICANT: Maurer, Karl-Heinz
TITLE OF INVENTION: New Beta-Glucanase from a Bacillus
FILE REFERENCE: #100BlpCT/US
CURRENT APPLICATION NUMBER: US/09/463,862A
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: DE 197 32 751.6
PRIOR APPLICATION NUMBER: PCT/EP98/04564
PRIOR FILING DATE: 1997-07-30
PRIOR FILING DATE: 1998-07-21
PRIOR FILING DATE: 1998-07-21
SOFTWARE: Patentin Version 3.1
SEQ ID NO 1
                                       DB 21;
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                          Score 266.5; DB 21;
Pred. No. 1.1e-18;
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TYPE: PRT
ORGANISM: Brevibacillus brevis
                                         20.0%;
36.0%;
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Best Local Similarity
                                         Query Match
Best Local Similarity
US-09-791-537-106873
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APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
SOFTWARE PATENTIN VERSION 3.0
SEQ ID NOS: 153055
SOFTWARE PATENTIN VERSION 3.0
LENGTH: 214
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debc, Derek
APPLICANT: Debc, JOseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 106873
LENGTH: 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 VSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGSDFTL 184
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                                  145 TEGGQVSNLTGTQGLRFNLMSSSSAAWVGQFDESKLPLFQFINWVKYKTTPGQGEGSD
                                                                                                  FTLDWTDNFDTFDGSRWGKGDWTFDGNRVDLTDKNIYSRDGMLILALTRXGQESFNGQVP
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                                                                                                                                                                                                                                                                                       RESULT 5
US-09-791-537-145019
Sequence 145019, Application US/09791537
GENERAL INFORMATION:
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ORGANISM: Brevibacillus brevis
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Matches 77; Conservative
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; ORGANISM: pdb 1CPM
US-09-791-537-145019
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Gaps

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APPLICANT: Bloomix, Inc.
APPLICANT: Bloomix, Inc.
APPLICANT: Bobb, Derek
APPLICANT: Debb, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SGCTWARE: PatentIn version 3.0
ERO ID NO 117361
LENGTH: 214
                                                                                                                                                                                                                                                                                                                                                                        67 GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                              127 VSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKV-----YKYTPGQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 AADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVG 150
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                                                                                                                                                                                                                                                                                                            1 FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGP---AHGTQWDEIDIEFLGKDT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 SGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSP 92
                                                                                                                                                                                                Length 394;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 G-----EGGSDFTLDWTDNFDTFDGSRWGKGD-------WTFDGN 208
                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                      90;
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                                                                                                                                                                                            18.8%; Score 250.5; DB 2 29.6%; Pred. No. 9.3e-17; Live 33; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.6%; Score 247.5; DB 32.9%; Pred. No. 8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 132244
LENGTH: 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLT--DKNI-YSRDGMLILALTRKGQESFN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 117361, Application US/09791537
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                  Similarity
                                                                                                                                      ; ORGANISM: pdb 1AXKA
US-09-791-537-132244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: pdb lAJKA
US-09-791-537-117361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-09-791-537-117361
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                                                                                                                                                                                              Query Match
Best Local S
Matches 68
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Best Local S
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GENERAL INFORMATION:
APPLICANT: Bionomix. Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6910, Application US/09791537
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
FILE REFERENCE: 261/210
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                                                                                                                                                                                                                                                                            PGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 VSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGSDFTL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                            6 DFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                        13;
                                                                                                  Length 308;
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                                                                                                                                                                                                                                                                                                                                126 QVSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP 173
                                                                                                                                                                                                                                                                                                                                                          209 -TENIPQTPQKIMMNLWPGIGVDGWTGVFDGEDTPVVTEYDWV---RYTP 254
                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                  DB 18;
                                                                                              Query Match 19.3%; Score 257.5; DB 18; Best Local Similarity 36.5%; Pred. No. 1.2e-17; Matches 62; Conservative 22; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.2%; Score 256.5; DB 2
33.8%; Pred. No. 8.8e-18;
tive 29; Mismatches 95
                      ; TYPE: PRT
; ORGANISM: Bacillus alkalophilus DSM 9956
US-09-463-862A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
LENGTH: 208
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Matches 77; Conservative
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; ORGANISM: pdb 1CPN
US-09-791-537-6910
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    LENGTH: 308
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US-09-841-132-192
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-417-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 192 LENGTH: 848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.8%;
Best Local Similarity 22.1%;
Matches 30; Conservative 7
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Chlamydia -09-841-132-192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL
FILE REFERENCE: 210121.469C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/841,132 CURRENT FILING DATE: 2001-04-23
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CURRENT FILING DATE: 2002-01-07
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 191 DTFDG 195
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                                761 --- VNSLGISYAW-EAYRKVEGGAVQLLEAGFDWEGAPMDLPRQELRVALENNTEWSSYF 816
                                                                                                                                                                             659 ETQNDMKTRYGVLGESSASWTSRGVL----ADALVEYRSLVGPVRPT---FYALHFNP-Y 710
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                                                                                                                                                                                                                     50
                                                                   FQFIN-----WVKVYKYTPGQG----EGGSDF----
                                                                                                       VEVSYASMKFPGFTEQGREARSFEDASLTNITIPLGMKFEL----AFIKGQFSE-----
                                                                                                                                           VR-----WTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSESAAWVGQFDESKLPL 159
                                                                                                                                                                                                                 DGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNY 109
                                                                                                                                                                                                                                                   AGVDIQLMEDFVLGVSGAAFLGKMDSQKFDAEVSRKGVVGSVYTGFLAGSWFFKGQYSLG 658
                                                                                                                                                                                                                                                                                     SGAELYTLEEVQYG------KFEARMKMAAASGTVSSMFL----YQNGSEIA 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAAWV------GQFDESKLPLFQFINWVKVYKYTPG-----QGEGGSDFTLDWTD 188
                                                                                                                                                                                                                                                                                                                             50;
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                              5.8%;
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Pred. No. 3
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                                                                     --TLDWTDNF 190
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Query Match
Best Local Similarity
Watches 50; Conserv.
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US-10-007-693-98
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US-09-841-132-178
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                                                                                                            ; ORGANISM: Chlamydia trachomatis serovar D US-10-007-693-98
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US-09-841-132-178
                                                                                                                                               ; SEQ ID NO 98
; LENGTH: 1531
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 178
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Patent No. US20020146776A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. US20020061848A1
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                                                      Query Match
Best Local Similarity
                                      Matches
                                                                                                                                                                                                                                                                       APPLICANT: Bhatia, Ajay
APPLICANT: Probst, Feter
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/007,693 CURRENT FILING DATE: 2001-12-05
                                                                                                                                                                                                                                                               FILE REFERENCE: 210121.515C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/841,132 CURRENT FILING DATE: 2001-04-23
                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1341 ETQNDMKTRYGVLGESSASWTSRGVL----ADALVEYRSLVGPVRPT---FYALHFNP-Y 1392
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 SGAELYTLEEVQYG -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VR-----WTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSESAAWVGQFDESKLPL 159
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                                                      5.8%;
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                                                      Score 83.5;
Pred. No. 20;
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Pred. No. 20;
 ---KFEARMKMAAASGTVSSMFL----YQNGSEIA 49
                                  Mismatches
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                                                                       DB 12;
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                                    Indels
                                                                     Length 1531;
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                                  Gaps
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RESULT 10 US-09-738-363-4

Sequence 4, Application US/09738363
Patent No. US20010010932A1
GENERAL INFORMATION:

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                                         1140
                                                                                                              1080
145 SAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGSDFTLD------WTDNFDTFD 194
                                                                           87
                                                                                                                                              33 SGTVSSMFLYQNGSEIA-----DGRPWVEVD-IEVLGKNPGSFQSNIITGKAGAQKTSEK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY, AGENT INFORMATION:
NAME: Sanders, Jay
REGISTRATION NUMBER: 39,355
REGISTRATION NUMBER: MA-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-372-8100
TELEPAX: 352-372-5800
                                                                                                                                                                                                                                                                         CLONE: E. col1 NM522(PMYC 1628) NRRL B-18652 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: YES ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Nematicidal Proteins NUMBER OF SEQUENCES: 40
                                   HNG------HFTKDAANWTVEG-----DAHQVVLEDGKRVLRLPDWSSSVS 1179
                                                                       HHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSS--E 144
                                                                                                           NGSIRSDISYQNIDAIVLPTLPKLRHWFMSDRFSEQGDIMAKFQGALNRAYAQLEQNTLL 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                      56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INT APPLICATION DATA:
APPLICATION NUMBER: US/09/738,363
FILING DATE: 15-Dec-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/076,137 FILING DATE: 12-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1289 amino acids
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                                                                                                                                                                                    Conservative
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                                                                                                                                                                                %; Score 85.5; D:
%; Pred. No. 11;
31; Mismatches
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                                                                                                                                                                                    ; 68
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                                                                                                                                                                                  Indels
                                                                                                                                                                                  65;
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Sequence 4, Application US/10042417
Patent No. US20020123082A1
GENERAL INFORMATION:

APPLICANT: Pagano, N TITLE OF INVENTION: TITLE OF INVENTION:

METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS

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RESULT 12
US-10-042-417-4
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SEQ ID NO 6377
LENGTH: 714
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 7059
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                                                                       603 ---- VEQSGKDSWITAVDNNEAFPEHR----- FQIDHVAVDIESDSV 640
                                                                                                           171 YTPGQGEGGSDFTLDWTDNFDTFDGSRWGKGDWTFDGNRVDLTDKNI 217
                                                                                                                                              553
                                                                                                                                                                                  116
                                                                                                                                                                                                                  495 TEFYSSRVNTQYSAVHLGCAGNRPEMKLRQMEMEESMFGD--WHDWGVEVFDGQIVFTID 552
                                                                                                                                                                                                                                                                                          436 YSSARVH-LPEIPAGNFRLTVRARAQSEELVDGVRPAIWMQNNTNFCADNDGRPYGELDI 494
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                                                                                                                                                                              GQEV----RKTEGGQVSNLTG-TQGLRFNLWSSESAAWVGQFDESKLPLFQFINWVKVYK 170
                                                                                                                                                                                                                                                                                                                           FSGAELYTLEEVQYGKFEARMKMAAAS-----GTVSSMFLYQNGSEIA--DGRPWVEVDI 59
                                                                                                                                              GKAVTSSGKDVFGNSVTPAAAPLRPAHFKLSEEEYREVIGQ-----PWHLILNTM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S 252
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                                                                                                                                                                                                                                         -EVLGKNPGSFQSNIITGKAG---AQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVD 115
                                                                                                                                                                                                                                                                                                                                                                   51;
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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YOKOI, HARUHIKO
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SENOH, AKIHIRO
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RESULT 8
US-09-738-363-2
; Sequence 2, Application US/09738363
; Patent No. US20010010932A1
; GENERAL INFORMATION:
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-818-247-22
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Best Local Similarity
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                                                                                                                  REFERENCE/DOCKET NUMBER: MA-20CCCD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEPAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/738,363
FILING DATE: 15-Dec-2000
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            APPLICATION NUMBER: 09/076,137
FILING DATE: 12-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Nematicidal Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Schnepf, Harry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SEEDLNGAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GEG-GSDFTLDWT----DNFDTFDGSRWGKGDWTF-DGNRVDLTDKNIYSRDGMLIL 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIVLTQSPSTLSASIGDRVTITCRASEGIYHWLAWYQQKPGKAPKLLIYKASSLASGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTRKGQESFNGQVPRDDEPAPNSSSVDKLAAALEHHHHHH 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {\tt RFSGSGSGTDFTLTISSLQPEDFATYYCQHYDSTPPTFGQGTKVDI--KRAAAEQKLI--}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KHHAVSP-----AADQAFHTYGLEWTPN--YVRWTVDGQEVRKTEGGQVSNLTGTQGLRF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLSCAASGFTFSSYAMSWVRQAPGKGLEWVSA---ISGSGGSTYYADSVKGRFTISRDNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Gainesville
STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st St
                                                  STRANDEDNESS:
                                                                TYPE: amino acid
                                                                                 LENGTH: 1385 amino acids
                                                                                                                                                                                                          REGISTRATION NUMBER: 39,355
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF SEQUENCES: 40
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                                                                                                                                                                                                                        Sanders, Jay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schnepf, Harry E. Schwab, George E. Payne, Jewel M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Narva, Kenneth E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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19.2%;
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Pred. No.
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CLONE: E. coli NM522(PMYC 1627) NRRL B-18651; SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-738-363-2
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US-09-215-450-26
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US-09-215-450-26
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Best Local Similarity
"-+-hes 56; Conserv:
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 26

LENGTH: 406

TYPE: PRT
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APPLICANT: Giese, Klaus
APPLICANT: Sin, Hong
APPLICANT: Xin, Hong
TITLE OF INVENTION: METASTATIC BREAST AND COLON CANCER REGULATED GENES
FILE REFERENCE: 1451.1(0) / 210030.447
FILE REFERENCE: 1451.1(0) / 210030.447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26, Application US/09215450 Patent No. US20020068278A1
                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 198-12-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1274 --VSQMIE----IENFNPDKEYNLVFHGQGEG--TVTLEHGEETKYIETHTHHFANFTT 1324
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                                    237
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                                                                                                         177 VTEMPALPFMLAEFDGVVGMGFIEQAIGRVTPIFDNIISQGVLKEDVFSFYYNRDSENSQ 236
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les 63; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
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RKGQESFNGQVPRDDEPAPNSSSVDKLAAAL 260
                                                                                                                                                                                                                                                                                             MKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AWVGQFDESKLPLFQFINWVKVYKYT-PGQGEGGSDFTLD------WTDNFDTFDG 195
                                  SLGGQIVLGGSD-POHYEGNFHYINLIK--TGVWQIQMKGVSVGSSTLLCEDG--CLALV 291
                                                                                                                                                                                  CSRLYTACVYHKLFDASDSSSYKHNGTELTLRYSTGTVSGFLSQDIITVGGTTVTQMFGE 176
                                                                                                                                                                                                                                                         MKRLTLGNTTSSVIL ----TNYMDTQYYGEIGI---GTPPQTFKVVFDTGSSNVWVPSSK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQ--RQGLTFESNKVTVT---ISSEDGEFLVDNIALV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSESA 146
                                                                       -----GGSDFTLDWTDNFDTFDGSRWGKGDWTFDGNRVDLTDKNIYSRDGMLILALT 229
                                                                                                                                            ---TQGLRFNLWSSESAAWVGQFDES---KLPLFQFINWVKVYK-----YTPGQGE--- 177
                                                                                                                                                                                                                     -----HAVSPAADQAFHTY-GLEWTPNYVRWTVDG---QEVRKTEGGQVSNLTG- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: BACILLUS THURINGIENSIS
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23.2%;
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                                                                                                                                                                                                                                                                                                                                                   Score 86.5;
Pred. No. 2;
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Pred. No. 7
                                                                                                                                                                                                                                                                                                                                  Mismatches 115;
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                                                                                                                                                                                                                                                                                                                                                                      DB 10;
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                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                   Length 406;
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                                                                                                                                                                                                                                                                                                                                  59;
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; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORCANISM: Homo Sapiens
US-09-804-626-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09804626 Patent No. US20020128190A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Caplan, Michael
TITLE OF INVENTION: Passive Desensitization
FILE REFERENCE: 200284-0103
CURRENT APPLICATION NUMBER: US/09/731,221
CURRENT FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 79
                                                                                                                                                                      Query Match
Best Local 9
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 79, Application US/09731221 Patent No. US20020018778A1
                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                   APPLICANT: Lobel, Leslie
APPLICANT: Lustbader, Joyce
APPLICANT: Lustbader, Joyce
TITLE OF INVENTION: EXPRESSION OF PROPERLY FOLDED AND SOLUBLE EXTRACELLULAR DOMAIN OF
TITLE OF INVENTION: GONADOTROPIN RECEPTOR
FILE REFERENCE: 0575/62259/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/804,626
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 526
   365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              491 KNNNPFKFFVP-PSQQSPRAVAVDKLAAALEHHHHHH 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 KGQESFNGQVPRDDEPAPNSSSVDKLAAALEHHHHHH 267
                                                                                                                                                 y Match 6.7%; Score 97; DB Local Similarity 22.3%; Pred. No. 0.3; hes 60; Conservative 33; Mismatches
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                                       79
                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
GA--TGPKTLDISSTKLQALPSYGLE-----
                                   GAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRF 138
                                                                        YGNGFEEVQSHAFNGTTLTSLELKEN--------VHLEKM--HNGAFR------ 364
                                                                                                             YGK-FEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQSNIITGKA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEWTPNYVRWTVDGQEVRKTEG---GQVSHLTGTQGLR---FNLWSSESAAWVGQFDE-- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REKLSDIPTSMYVDYVRVWEKSAG 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CEVNQNEIIWYVDGVEVARKPNKYWHRPMNVTLSLGLRKPFVKFFDNKNNAINPETDAKA 285
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Pred. No. 0.1
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                                                                                                                                                                  DB 10;
0.3;
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                                                                                                                                                                                  Length 518
                                                                                                                                                   Indels
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CURRENT APPLICATION NUMBER: US/09/818,247
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: WO PCT/US01/09699
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/192,197
PRIOR APPLICATION NUMBER: US 60/192,197
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 26
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-804-626-4
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APPLICANT: Lustbader, Joyce
APPLICANT: Lustbader, Joyce
TITLE OF INVENTION: EXPRESSION OF PROPERLY FOLDED AND SOLUBLE EXTRACELLULAR DOMAIN
TITLE OF INVENTION: GONADOTROPIN RECEPTOR
FILE REFERENCE: 0575/62259/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/804,626
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
                                           SOFTWARE: PatentIn Ver.
SEQ ID NO 22
LENGTH: 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22,
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                                                                                                                                                                                                                                                                                                                        APPLICANT: Mostov, Keith E.
APPLICANT: Chapin, Steven J.
APPLICANT: Richman-Eisenstat, Janice
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Ligands Directed to the No. US20020102657A1-Secretory Componen
TITLE OF INVENTION: No. US20020102657A1-Stalk Region of pigR and Methods of Use T
FILE REFERENCE: 18062E-000910US
ORGANISM: Artificial Sequence
                        TYPE: PRT
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38.2%;
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                                                                                                                               Matches
                                                                                                                                                  Best Local
                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 6:
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                                                       289 YGYYEARIKGASTFPGVSPAFWMYSTIDRSLTKEGDVQYSEIDVVELTQKSAVRESDHDL 348
20 YGKFEARMKMAAASGTVSSMF-LYQ--NGSEIADGR-PWVEVDI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/988,200 FILING DATE: 19-No. US20020094553A1-2001 PRIOR APPLICATION CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                      MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
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                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/269,731
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: FR 96 12204
FILING DATE: 07-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: VIRGINIA COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (703) 412-11
TELEFAX: (703) 412-1161
                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: DENNISON,
                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                            LENGTH: 620 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: IRA SCHULTZ
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                                                                                                                               Conservative
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INVENTION: Glycolyse hydrolase genes and their
use for producing enzymes for the biodegradation
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HENRISSAT, Bernard
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27.3%;
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                                                                                                                               23;
                                                                                                                                                Score 117; DB 10
Pred. No. 0.0055;
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Square 4, 1745 Jefferson Davi
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RESULT 3
US-09-988-200-8
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GENERAL INFORMATION:
                                                                                                                Matches
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                                                                                                                                                 Query Match
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                     108
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                                                                                                                                Local Similarity
63 -----GKNPGSFQSNI----ITGKAG-----AQKTSEKHHAVSPAADQAFHTYG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: <Unknown>
APPLICATION NUMBER: FR 96 12204
FILING DATE: 07-OCT-1996
ATTORNBY/AGENT INFORMATION:
NAME: IRA SCHULTZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BARBEYRON, Tristan
                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 412-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                          SEQUENCE DESCRIFTION: SEQ ID NO:
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                                                                      FSGAELYTLEEVQYGKFEARMKMA-AASGTVSSMFLYQN-GSEIADGRP-WVEVDIEVL- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WYVDGEIVGEKDNLYWHRQMNLTLSQGLRAPHTQWKCNQFYPSANKSAEGFPTSMEVDYV 457
                                   FTSGIFKSYQKFTYGYFEAKIQGADIGEGVCPSFWLYSDFDYSVANGETVYSEIDVVELQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19-No. US200 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/988,200 FILING DATE: 19-No. US20020094553A1-2001
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                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: <Unknown>
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                                                                                                                                                                                                                                                                                 LENGTH: 545 amino acids
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                                                                                                                Conservative
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INVENTION: Glycolyse hydrolase genes
use for producing enzymes
                                                                                                                                                                                                                                                                amino acid
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RICHARD, Christophe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HENRISSAT, Bernard
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                                                                                                            41;
                                                                                                            Score 113; DB 10;
Pred. No. 0.011;
11; Mismatches 78;
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                                                                                                                                                                                                                                                                                                                                                                                                    <Unknown>
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                                                                                                                                                 Length 545;
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the biodegradation of
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1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

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    GenCore version Copyright (c) 1993 - 2003
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10 US-09-731-221-79
10 US-09-804-626-4
10 US-09-818-247-22
10 US-09-818-363-2
10 US-09-738-363-2
10 US-09-738-363-7
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2 US-10-007-693-98
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US-09-813-718-16
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                           Sequence 152, App
Sequence 8, Appli
Sequence 79, Appl
Sequence 27, Appli
Sequence 22, Appli
Sequence 26, Appli
Sequence 26, Appli
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Sequence 47, Appli
Sequence 170, Appli
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APPLICANT:
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Renz, Andreas Ehrhardt, Thomas Reindl, Andreas Cirpus, Petra

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US-09-925-299-865	US-10-044-303-2	US-09-866-562-38	US-09-750-424-1	US-09-738-626-4312	US-09-734-569-150	US-09-949-192-6	US-09-728-911-2	US-09-833-435A-1	US-09-731-221-77	US-10-106-014-4	US-09-747-521-4	US-10-105-694-4	US-10-105-695-4	US-09-815-242-12138	US-09-815-242-5350	US-09-738-626-6052	US-09-864-761-42996	US-09-988-974-9	US-09-988-974-5	US-09-731-221-78	US-09-734-569-28	US-09-863-547B-1	US-10-098-174-1	US-09-813-718-10	US-09-813-718-12
86.	Sequence 2, Appli	Sequence 38, Appl	Sequence 1, Appli	Sequence 4312, Ap	Sequence 150, App	Sequence 6, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 77, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli		Sequence 5350, Ap	Sequence 6052, Ap		9	Sequence 5, Appli	Sequence 78, Appl	Sequence 28, Appl	Sequence 1, Appli	Sequence 1, Appli		Sequence 12, Appl

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Physcomitrella patens US-09-734-569-152
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1/WordPerfect 6.1
SEQ ID NO 152
LENCTH: 287
TYPE: PRT
                                                                                                                                                                                                                                               Query Match
Best Local :
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PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/734,569
CURRENT FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involv TITLE OF INVENTION: in the synthesis of carbohydrates FILE REFERENCE: BASF-NAE-1332-99-US
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123 VDGVGGRE-QQMYLGFDPSAD--FHYYRFRWSKDMVVFYVDNKPVR-----VFKNLEGTV 174
                                                                                                         69 YVDISAYIKMPPEDSAGTVTTFYMSSQGDQ-----HYELDMEFLGNTSGQPFLLHTNVF 122
                                                                                                                                                                                                                  / Match 8.3%; Score 120; DB 10; Length 287;
Local Similarity 23.0%; Pred. No. 0.0011;
nes 49; Conservative 30; Mismatches 70; Indels 6
                                                75 TGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGT- 133
                                                                                                                                                      20 YGKFEARMKMAA--ASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNPGS---FQSNII 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bischoff, Friedrich
Frank, Markus
Freund, Annette
Duwenig, Elke
Schmidt, Ralf-Michael
Reski, Ralf
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SEQUENCE FROM N.A.

MEDLINE-21608551; PubMed-11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Geloo C., Slater S.;
"Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
Science 294:2323-2328(2001).
EMBL; AE008376; AAL44856.i; ALT_INIT.

EMBL; AE008279; AAK89373.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 NPGSFQSN-IITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRKTVDGQEVRKTE 123
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Endo-1.3-1,4-beta-glycanase, ExoK.
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33.8%; Pred. No. 2.8e-08;
tive 27; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 14.3%; Score 206; DB 16; Best Local Similarity 35.1%; Pred. No. 8.9e-09; Matches 54; Conservative 26; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 AA
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DNA Res. 7:331-338(2000).
EMBL; AP003006; BAB51743.1; -.
INLECTPRO, IPPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLYVO_HASE16.
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STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
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SEQUENCE 293 AA;
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QY 123 EGGQVSNLTGTQGLRFNLWSSES-AAWVGQF 152

Db 225 DPAKLP--SHAQKIFFSLWGSETMKGWMGAF 253

Search completed: January 9, 2003, 12:18:12 Job time : 25.7951 secs

InterPro; IPR000757; Glyco\_hydro\_16

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Query Match
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                       RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Douette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing
                                                                                                                                                             67 GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                                                                                138 TKVQFNYYT---SGQGNHEYLYNLGFDASQGFHTYGFDWQADHITWYVDGRAVYTA---- 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSFQSNIITGKAGAQKTSEKH---HAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 TEVQFNYYTNGVG-----KHEYLYKLGFDASKGFHTYGYIWEQNYIAWLVDGKEVYRA- 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
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                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmioutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 246;
                                                                                                    Length 237;
                                                                                                                         69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73; Indels
                                                                  BETA-(1,3-1,4)-GLUCANASE.
7DEF5BCE53790470 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
SEQUENCE 246 AA; 27717 MW; COEBC302678D2FE1 CRC64;
                                                                                                                                                                                                                                                    127 VSNLTGTQG-LRFNLW--SSESAAWVGQFDESKLPLFQFINWV 166
                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.4%; Score 221; DB 16;
llarity 33.7%; Pred. No. 4.5e-10;
Conservative 19; Mismatches 73;
                                                                                                  16.0%; Score 230; DB 2;
33.1%; Pred. No. 8.1e-11;
tive 26; Mismatches 69;
                                 PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000757; Glyco_hydro_16.
PRIME; PR00722; Glyco_hydro_16; 1.
PRIME; PR00737; GLHVDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed-11466286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
EMBL; AE007778; AAK80751.1;
                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Last and Endo-1,3(4)-beta-glucanase family 16 CAC2807.
                                                                                                                                                                                                                                                                                                                     PRT;
         Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
                                                     1 24 PO
25 237 Bi
237 AA; 26989 MW;
                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 18, (TrEMBLrel. 18, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium acetobutylicum
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Local Sim.
58;
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01-OCT-2001
                                                                                                                         54;
                                                                            SEQUENCE
                                                                                                   Query Match
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                                           Signal.
                                                        SIGNAL
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SYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDIESL 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The genome of the natural genetic engineer Agrobacterium tumefaciens {\sf C58."};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-2160856; PubMed-11743193; Mooks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Mooks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kuyyavin T., Levy R., Li M.-J., McClelland B., Palmieri A., Kaymond C., Rouse G., Saenphimmechak C., Wu Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Endo-1,3-1,4-beta-glycanase.
Exox OR ATU4055 OR AGR_L_1600.
Agrobacterium tumefaciens (strain CS8 / ATCC 33970).
Bacterila: Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67; Indels 10;
                                                                                                                                                                                                                                                                                                      ROGIGUENCE FROM N.A.
ROGIGUEZ V., Mellado R.D.;
"Novel lichenases from soil.";
"Novel lichenases from soil.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF254960; AAK50613.1;
Interpro: IPRO00725; Glyco_hydro_l6.
Pfam; PF00722; Glyco_hydro_l6; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; UNKNOWN_1.
NOW_TER 205
SEQUENCE 205 AA; 22890 MW; E7CADAAFE02AZF51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 205;
                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.2%; Score 219; DB 2; 36.2%; Pred. No. 5.1e-10; tive 20; Mismatches 67.
205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 EGGOVSNLTGTQGLRFNLWSSESA-AWVGQFD 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 ATTOVPAAPGK -- IMMNLWNGTGVDDWLGSYN 197
                                                                                                                                                      Endo 1-3,1-4-beta-glucanase (Fragment)
uncultured bacterium.
Bacteria; environmental samples.
                                                                 Created)
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                                                       01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity 36.28 55; Conservative
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PRELIMINARY;
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140 GKDTTKVQFNYYTNGAG---NHEKIVDLGFDAANAYHTYAFDWQPNSIKWYVDGQ-LKHT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                             212 AA;
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Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          NCBI_TaxID=1406;
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01-JUL-1997
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                                                                                           RESULT 10
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9
                                                                                                                                                                   van Rensburg P., van Zyl W.H., Pretorius I.S.;
"Over-expression of the Saccharomyces cerevisiae exo-beta-1,3-
"Over-expression of the Saccharomyces cerevisiae exo-beta-1,4-
glucanase gene together with the Butyrivibrio fibrisolvens endo-beta-
1,4-glucanase gene and the Bacillus subtilis endo-beta-1,3-1,4-
glucanase gene in Saccharomyces cerevisiae.";
Submitted (JuN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U60830; AAB0759-1;
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HSSP; P27051; IGBG.
                                                                                                                                                                                                                                                                                                                                                                                                                               63 GKNPGSFQSNIITGKAGAQKTSEKHHAVSPA---ADQAFHTYGLEWTPNYVRWTVDGQEV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVFWTVDGQEVRKT 122
                                                                                                                                                                                                                                                                                                                                                                                                                SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62
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                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KHTATTQIPTAPGK -- IMMNLWNGTGVSDWLGSYNGVN-PLYAHYDWVRYTK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 242;
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Sun J., Li W., Gu S., Xu Z., Zhao H., Xiao J.;
Sun J., Li W., Gu S.), to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: AR490978: AAM08358.1; -
SEQUENCE 242 AA: 27238 MW: 285/FED3FE76AE69A CRC64;
                                                                                                                                                                                                                                                                          Interpro; IPR000757; Glyco_hydro_16.

Pfam: PF00722; Glyco_hydro_16; 1.

PRINTS; PR00737; GLYCOS_LIVE

PROSITE; PS01034; GLYCOS_LIVE

SEQUENCE 239 AA; 26969 MW; C4219760D13F878A CRC64;
           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Endo-beta-1,3-1,4-glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.2%; Score 232.5; DB 2;
llarity 34.9%; Pred. No. 5.2e-11;
Conservative 24; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                           16.3%; Score 234.5; DB 2 33.7%; Pred. No. 3.5e-11;
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Matches 58; Conservative
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nes 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus subtilis.
                                                                                                                                             SEQUENCE FROM N.A. STRAIN-NCIB 8565;
                                                                            Bacillus subtilis.
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                                                                                                                 NCBI_TaxID=1423;
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Matches
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67 GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          extracellular
                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Endo-1,3-1,4-beta-glucanase (Fragment).
Pannibacillus polymyxa (Bacillus polymyxa).
Bacteria; Firmtcutes; Bacillus/Clostridium group; Bacillales;
Paenibacillaceae; Paenibacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.0%; Score 230; DB 2; Length 212; 35.1%; Pred. No. 7e-11; ive 23; Mismatches 70; Indels
123 EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 VSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yao W., Wang Y., Song W., Yang K., Su Z.;
"Gene Cloning of an antifugal protein.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF284449; AAG02415.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Exinci M., Flint H.J.;

"Isolation and overexpression of a gene encoding an extra beta-(1,3-1,4)-glucanase from Streptococcus bovis JB1-';
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.

EMBL, 292911, CAB07443.1;

HSSP; P23904; IAJK.
                                  24127 MW; 7E707E7FBEF7A440 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P23904; IAJK.

IRCEPPO: IPRO00757; G1yco_hydro_16.

Pfam: PF00725; G1yco_hydro_16; 1.

PRINTS: PR00737; GLHYDRLASE16.

NON_TER: PS01034; GLYCOSYL_HYDROL_F16; 1.

NON_TER: 212 212
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NCBI_TaxID=1315;
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SEQUENCE FROM N.A.
Rodriguez V., Mellado R.P.;
"Novel lichenases from soil.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Best Local Similarity
Matches 60; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aurilia V., Martin J.C., Munro C.A., Mercer D.K., Flint H.J.; "Organisation and strain distribution of genes responsible for the utilization of xylans by the rumen cellulolytic bacterium Ruminococcus flavefaciens 17.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              691 TQVQFNYYTNGQGKH---EKLYDLGFDSSEAYHTYGFDWQPNYIAWYVDGREVYRA---- 743
112 GKDTTKVQFNYYTNGAG---NHEKLADLGFDAANAYHTYAFDWQPNSIKWYVDGQ-LKHT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Lachnospiraceae; Ruminococcus.
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                                          EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                                                  127 VSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Family 11 xylanase /family 16 beta (1,3-1,4) glucanase
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 20, Last annotation update)
Endo 1-31-4-beta-glucanase (Fragment).
uncultured bacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.9%; Score 242.5; DB 34.9%; Pred. No. 4e-11; tive 21; Mismatches
                                                                                                                                                                                       802 AA
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                                                                                                                                                                                                                                                                                                                                Ruminococcus flavefaciens
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                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 11; Gaps
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**RODINGE FROM N.A.

**RODINGE FROM N.A.

**RODINGE V., Mellado R.P.;

**RODINGE V., Mellado R.P.;

**Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

**REMBL, AF24959; AAK50612.2; -.

**R InterPro; IPR000757; Glyco_hydro_16.

**R PRINTS; PR00737; GLHYDRLASE16.

**R PRINTS; PR00737; GLHYDRLASE16.

**R PROSITE; PS01034; GLYCOSYL_HYDROL_F16; UNKNOWN_1.

**INON_TER**

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 ATTQIPAAPGK--IMMNLWNGTGVDDWLGSYNGVN-PLYAHYDWVRYTK 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
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EMBL; AF24961; AAK50614.2; -.
InterPror; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; UNKNOWN_1.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.4%; Score 235.5; DB 2; ilarity 35.5%; Pred. No. 2.5e-11; Conservative 23; Mismatches 75;
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01-DEC-2001 (TrEMBLrel. 19, Last seque
01-MAR-2002 (TrEMBLrel. 20, Last annot
Endo 1-3,1.4-beta-glucanase (Fragment)
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
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uncultured bacterium.
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                                                                                                                                              STRAIN=137;
MEDLINE=94288605; PubMed=7517127;
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                                   Bacillus
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                                                                                                                SEQUENCE FROM N.A.
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                                                           NCBI_TaxID=1409;
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SEQUENCE
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Q93GE8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | : | : | : | : | 326
SGDDNEEEPVEEVEEPAEDEEVSVRPIGSAIYETFNTFNEDIWSIAHGWT-NGQMFNAT 326
APPYKAGELRINDFYQYGLPEVSMKPAKVEGTVSSFFTY-TGEWDWDGDPWDEIDIEFLG 157
                                                                                     KNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTE 123
                                                                                                                                              KDTTRIQFNYFTNGVGG---NEFYYDLGFDASESFNTYAFEWREDSITWYVNGEAVHTA- 213
                                                                                                                                                                                                   GGQVSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP----GQGE 177
                                                                                                                                                                                                                                                                                                                   ---TENIPQTPQKIMMNLWPGVGVDEWTGVFDGDNTPLHADYEWV---RYTPLEALDEEE 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIANGRPWVEVDIEVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTEGGQVSNLTGTQG-LRFNLWSSESAA--WVGQFDESKLPLFQFINWVKVYKYTP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-ATCC21367;
Lee D.-S., Kim J.-Y., Kim H.-B.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databasses.
EMBL; AF306531; AAG53947.1; -
HSSP; P23904; LATK.
InterPro; IRR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRASE16.
PROSITE; PS01034; GLYCOSYL, HYDROL_F16; 1.
SEQUENCE 256 AA; 27604 MW; 989E50C09F6E4531 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Endo-beta-1,3-1,4-glucanase.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 17.3%; Score 248.5; DB 2; Best Local Similarity 34.7%; Pred. No. 2.9e-12; Matches 61; Conservative 28; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                    -- DKNIYSRDGMLILALTRKGQESFNGQVPRDDEPA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----- DDEEA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327 WYDSQITFSNGIMRFAIDKE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 17,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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SEQUENCE FROM N.A.
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Bacillus sp.
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Tabernero C., Coll P.M., Fernandez-Abalos J.M., Perez P.,
Santamaria R.I.;
Santamaria R.I.;
"Cloning and DNA sequencing of bgaA, a gene encoding an endo-beta-1,3-
"L, 4-glucanase, from an alkalophilic Bacillus strain (N137).",
Appl. Environ. Microbiol. 60:1213-1220(1994).
EMBL, 212151, CAA78135.1;
HSSP: P23904; 1AJK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 TENIPQTPQKIMMNLWPGIGVDGWTGRFNGEDTPVVTQYDWV---KYTP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 VSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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    SIĞNAL
    1
    31
    POTENTIAL.

    CHAIN
    32
    276
    LICHENASE.

    SEQUENCE
    276
    AA, 31770 MW; D047F8A34CA9EBE2 CRC64;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 AA; 24159 MW; 3DB186D3B9D991CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.2%; Score 247.5; DB 2; 36.1%; Pred. No. 3.9e-12; attive 20; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 AA
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                                                                                                                                                                                                                          InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
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9

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Q9fill arabidopsis

Q80803 arabidopsis

Q80803 arabidopsis

Q9m0d1 arabidopsis

Q9mxn1 thermotoga

Q44449 arabidopsis

Q60039 thermotoga

Q8910 arabidopsis

Q8446 arabidopsis

Q9440 arabidopsis

Q9401 aspergillus

Q9420 trichoderma

Q9420 trichoderma

Q9420 trichoderma

Q9420 trichoderma

Q9420 arabidopsis

Q9420 arabidopsis

Q9420 arabidopsis

Q9421 crichoderma

Q9421 fagus sylva

Q9420 arabidopsis

Q9421 cricholum

Q8471 clostridium

Q8471 clostridium

Q8471 arabidopsis

Q9473 clostridium

Q8471 arabidopsis

Q9473 arabidopsis

Q9473 arabidopsis

Q9474 orabidopsis

Q9474 orabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takami H., Nakasone K., Pakaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K., Complete genome Sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).

EMBL; APAD01518; BAB069551.1; -

HSSP; P23904; IAJK.

InterPro: IPR000757; Glyco_hydro_16.

InterPro: IPR00199; Gram_pos_anchor.

Pfam; PF0072; Glyco_hydro_16: 3.

Pfam; PF0072; Glyco_hydro_16: 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16; Length 851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 18.5%; Score 266.5; DB 16; Length Local Similarity 29.7%; Pred. No. 5.1e-13; les 82; Conservative 31; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Endo-beta-1,3-1,4 glucanase (licheninase) (EC 3.2.1.73)
BGLS OR BH233.
Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00737; GLHVDRLASE16.
PROSTITE; PS01034; GLYCOSYL_HYDROL_F16; 3.
Hydrolase; Glycosidase; Complete proteome.
SEQUENCE 851 AA; 98142 MW; C1C4F0F158400285 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            851 AA
                    Q9F131
O80803
Q9M0D1
Q9WXN1
Q94A49
O42800
Q60039
                                                                                                                                                                           Q38910
Q9FKL8
Q9FKL8
Q9GZU4
Q9H420
Q9ZRV1
Q38907
Q38907
Q9SEB0
Q9SEB0
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Q39118
Q33012
Q38857
Q9FKL9
O68641
Q05790
Q8S902
P93669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINE=20512582; Pubmed=11058132;
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157.5
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Q9K7X5;
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  δλ
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093qe8 uncultured
093qe7 uncultured
093qe7 uncultured
04561 bacillus su
087mp0 bacillus su
09fdc9 paenibacill
00786 streptococc
097fd3 clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8u8n5 agrobacteri
Q98c78 rhizobium l
Q9k7x6 bacillus ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9k7x5 bacillus ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29apd8 bacillus ci
                                                                                                                                                             (without alignments)
2312.009 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                      9, 2003, 12:13:37; Search time 23.7951 Seconds
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                                                                                                                                                                                                                                                        1 MVSAKDFSGAELYTLEEVQY.......PNSSSVDKLAAALEHHHHH
                    GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                         671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                               protein search, using sw model
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Q9APD8
Q45648
Q93GE8
Q93GE7
Q93GE6
Q45691
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
sp_mammal:*
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sp_virus:*
sp_vertebrate:*
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sp_phage:*
sp_plant:*
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sp_bacteriap:*
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length: 2000000000
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sp_bacteria:*
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sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                                                                                                                                                                                              107 FEFLGNISGHPYTLHTNVYY-KGTGDKEQQFHLWFDPTVN--FHTYCTTWNPQRIJFTVD 163
                                                                                                                                                                                                                                                                                                                                                                                           ::| ||: ::| ||| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  251
                                                                                                                                                                                                                                                                                                                                                                    GQEVRKTEGGQVSNL--TGTQGLRF--NLWSSESAAWVG---QFDESKLPLFQFINWVKV 191
                                                                                                                                                                   Gaps
                                                                                                                                                                                                       24 NVSAKDFSGAELYTLEEVQYGKFEARMKMAA--ASGTVSSMFLYQNGSBIADGRPWVEVD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                192 YKYTPGQGEGGSDFTLDWTDNFDTFDGSRWGKGDWTFDGNRVDLTDKNTYSRDGMLILAL
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                                                                                                                         9.5%; Score 173; DB 23; Length 282; 25.6%; Pred. No. 2.3e-06; Live 36; Mismatches 92; Indels 5
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990S-0132484.
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Matches 64; Conservative
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                                                                                   282 AA;
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
19-APR-1999;
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28-JUL-1999;
02-AUG-1999;
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25-OCT-1999;
26-OCT-1999;
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15-SEP-1999;
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113-AUG-119
113-AUG-119
116-AUG-119
117-AUG-119
118-AUG-119
118-AU
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03-AUG-19
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06-AUG-19
09-AUG-1
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29-SEP-19
04-OCT-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                        SISLDKSSGSGFQSNQEFLYGKAEVQMKLVPGNSAGTVTTFYLK-----SPGTTWDEID 106
                                                                                                                                                                                                                  82 IEVLGK----NPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVD 138
                                                                                                                                                                                                                                                                         GQEVRKTEGGQVSNL--TGTQGLRF--NLWSSESAAWVG---QFDESKLPLFQFINWVKV 191
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                                                                                                                                Gaps
                                                                                                                                                         24 NVSAKDFSGAELYTLEEVQYGKFEARMKMAA--ASGTVSSMFLYQNGSEIADGRPWVEVD 81
                                                                                                                                                                                                                                  218 YR------L YRNV-DGCVWANGKSSCSANSPWFTQK------L
                                                                                                                              58;
                                                                                               Length 282;
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                                                                                                                              Indels
                                                                                               9.5%; Score 173; DB 21;
25.6%; Pred. No. 2.3e-06;
live 36; Mismatches 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herbicidal; plant; agriculture; herbicide
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                                                                                                                           36;
          990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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                                                                                                                             64; Conservative
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                                                                                                               Best Local Similarity
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                      21-MAY-1999;
24-MAY-1999;
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 9
                                                                                                                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                           82 IEVLGK---NPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVD 138
                                                                                                                                                                              GOEVRKTEGGOVSNL--TGTQGLRF--NLWSSESAAWVG---QFDESKJPLFQFINWVKV 191
                                                   Gaps
                                                                                                                                                                                             NVSAKDFSGAELYTLEEVQYGKFEARMKMAA--ASGTVSSMFLYQNGSEIADGRPWVEVD
                                                 98; Indels 24;
                         Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 39167.
                        ; Score 185; DB 23;
; Pred. No. 2.3e-07;
34; Mismatches 98;
                                                                                                                                                                                                                                192 YKYTPGQGEGGSDFTLDWTDNFDTFDGS----RWGK 223
                                                                                                                                                                                                                                                        DACVWSNGKSSCSANSSWFTQVLDFKGKNRVKWAQ 258
                                                                                                                                                                                                                                                                                                                        AAG32464 standard; Protein; 282 AA
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9905-0123180

9905-0125788

9905-0126785

9905-0126785

9905-0128234

9905-0128234

9905-0128714

9905-013845

9905-013049

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9905-0131449

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9905-0131449
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27.4%;
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99US-0134218.
99US-0134219.
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99US-0134370.
99US-0134768.
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                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
                                    Local Similarity
les 59; Conserv
282 AA
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14-MAY-1999;
18-MAY-1999;
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 Sequence
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                         Query Match
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                                                   Matches
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99US-0149723.
99US-0149723.
99US-0149929.
99US-01499029.
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99US-0151930.
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99US-0150884.
99US-0151065.
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99US-0151080.
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10-AUG-1999

11-AUG-1999

113-AUG-1999

13-AUG-1999

13-AUG-1999

13-AUG-1999

13-AUG-1999
                                             02-AUG-1999;
03-AUG-1999;
04-AUG-1999;
04-AUG-1999;
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25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
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117-AUG-11
18-AUG-11
18-AUG-11
20-AUG-11
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27-AUG-11
27-AU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                               SISIDKFSGSGFQSHQEFLYGKVEVQMKLVPGNSAGTVTTFYLK-----SPGTTWDEID 106
                                                                                                                                                                                                                                        164 GIPIREFKNSEALGVPFPKHQPMRLYASLWEAEHWATRGGLEKTDWSKAPFTAFYRNYNV 223
                                                                                                                                                                                                                                                                                 GQEVRKTEGGQVSNL--TGTQGLRF--NLWSSESAAWVG---QFDESKLPLFQFINWVKV 191
                                                                                                                                    Gaps
                                                                                                                                                                8
                                                                                                                                                                24 NVSAKDFSGAELYTLEEVQYGKFEARMKMAA--ASGTVSSMFLYQNGSEIADGRPWVEVD
                                                                                                                                                                                                                       82 IEVLGK---NPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVD
                                                                                                                                   24;
                                                                                                     Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; SEQ ID NO 2948; 261pp + Sequence Listing; English.
                                                                                                                                    Indels
                                                                                                                                    98;
                                                                                                   Score 185; DB 21;
Pred. No. 2.3e-07;
4; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herbicidally active polypeptide SEQ ID NO 2948.
                                                                                                                                                                                                                                                                                                                                          192 YKYTPGQGEGGSDFTLDWTDNFDTFDGS---RWGK 223
                                                                                                                                                                                                                                                                                                                                                                    224 DACVWSNGKSSCSANSSWFTQVLDFKGKNRVKWAQ 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herbicidal; plant; agriculture; herbicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB93737 standard; Protein; 282 AA.
                                                                                                   10.1%; Scor
27.4%; Preditive 34; 1
               990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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                                                                                                                    Local Similarity 27.49
nes 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tietjen K, Weidler M;
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26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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                                                                                                      Query Match
Best Local S
Matches 59,
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19 - MAY - 1999;
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01 - JUN - 1999;
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08-JUL-1999;
09-JUL-1999;
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27-JUL-1999;
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19-JUL-1999;
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21-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                    DIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQ 140
                                                                                                                                                                                                                                                              DIEFLGYDTTKVQFNYYTNCQGHH---EHIHYLGFDASQGFHTYGFFNARNSITWYVDGT 192
                                                                                                                                                                                                   79 LTIDRDGSGYTCGEYRTKNYYGYGMFQVNMKPIKNPGVVSSFFTYTGP3---DGTKWDEI 135
of grain (e.g. barley or wheat) in the brewing and fermentation industries to increase carbon substrate availability and to maximise production of desired products.
                                                                                                                                 87; Indels 13; Gaps
                                                                                                                                                                   21 LITINVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEV 80
                                                                                                   DB 19; Length 245;
                                                                                                                                                                                                                                                                                                    141 EVRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWV 189
                                                                                                                                                                                                                                                                                                                         193 AVYTA----YDNIPDTPGKIMMNAWNGIGVDDWLRPFN-GRINISAYYDWV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 61207.
                                                                                               Query Match 10.4%; Score 190.5; DB 1
Best Local Similarity 31.6%; Pred. No. 6.5e-08;
Matches 54; Conservative 17; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                      AAG48467 standard; Protein; 282 AA
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990S-0126264
990S-0128746
990S-01280314
990S-0139047
990S-0130047
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99US-0125788.
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                                                                   245 AA;
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05-MAR-1999,
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25-MAR-1999,
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06-MAY-1999,
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-MAY-1999;
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                                                                   Sequence
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03-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-1998
                                                                                                                                                                                                                                                                         AAW37884;
                                          Seguence
                                                            Query Match
                      AAQ05833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen H,
                                                                       Best Local
                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                Matches
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                                                                                                                                                                                                                                            AAW37884
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/label=amino-terminal half of B.macerans beta-glucanase
                                                                                                                                          EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
                                                                                                                                                       131..234
/label-carboxyl-terminal half of B.amyloliquefaciens
                                                                                 Gaps
                                                                                                   23 TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI 82
protein accumulates in the ripe (but ungerminated) seeds. The proportion of these to malted seeds is increased therefore, without an unacceptable increase in viscosity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vonwettstein D;
                                                                                                                                                                                143 RKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 195
                                                                                                                                                                                             New thermostable (1,3-1,4)-beta-glucanase - prepd. using hybrid gene obtd. using Bacillus amyloliquefaciens and B.macerans genes
                                                                                                                                                                                                                                                                                                                                  Hybrid pre-beta-glucanase; glucans; beer; animal feed; poultry.
                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This hybrid protein is encoded by the beta-glucanase-H2 gene. Following processing of the signal peptide the mature protein is produced, comprising the amino terminus of the B.macerans beta-glucanase and the carboxyl.terminal half of the B.amylo-liquefaciens beta-glucanase. This hybrid protein is thermostable and hydrolyses beta-glycosidic linkages in (1,3-1,4)-beta-glucans. Reducing sugars are obtd. at high temps. and
                                                            DB 11; Length 237;
                                                                               74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olsen O,
                                                           12.5%; Score 228; DB 11
34.3%; Pred. No. 4.4e-11
ive 25; Mismatches 7.
                                                                                                                                                                                                                                                                                                                                                      Bacillus amyloliquefaciens, Bacillus macerans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borriss R, Hofemeister J, Thomsen KK,
                                                                                                                                                                                                                                                                                                                                                                                                                         beta-glucanase
                                                                                                                                                                                                                                                                                                              Hybrid (1,3-1,4)-pre-beta-glucanase.
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; page 28; 84pp; English.
                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                   AAR06622 standard; protein; 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CARL-) CARLSBERG A/S.
(DEAK ) AKAD WISSENSCHAFT DDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90WO-DK00044,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89DK-0003848.
89DD-0325800.
                                                                                                                                                                                                                                                                                            (first entry)
                                                                               60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1990-275129/36.
N-PSDB; AAQ05833.
                                                                     Best Local Similarity
                                        237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9009436-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-AUG-1989;
16-FEB-1989;
                                                                                                                                                                                                                                                                                            09-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-AUG-1990.
                                        Sequence
                                                            Query Match
                                                                                                                                                                                                                                                                       AAR06622
                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                        83
                                                                                                                                                            132
                                                                                                                                                                                                   188
                                                                               Matches
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This sequence is the lichenase (licA) of Orpinomyces sp. strain PC-2 of the invention. The protein was purified from a fungus or a fungal culture or from a recombinant DNA molecule having a fungal lichenase coding sequence. The lichenase enzyme hydrolyses the beta-1,4-glucan bonds adjacent to beta-1,3-linked glucan bonds, but does not cleave beta-1,4-linked glucans. They can be used for the treatment of animal grain-containing feeds to improve nutrient availability and for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
                                                                                                                                                                                                                                                                                                                                                                                   75 TSSAYNKFDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGP---AHGTQWDEIDI 131
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                           23 TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lichenase; licA; fungus; enzyme; beta-1,4-glucan bond hydrolysation; beta-1,3-linked glucan bond; grain-containing feed; grain treatment; nutrient availability; brewing; fermentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated lichenase protein - is obtained from Orpinomyces PC-2, used for treatment of grain to improve feeds or to improve brewing
                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                             DB 11; Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 193
      prods., e
See also
thus this enzyme can be used in the mfr. of food beer and animal feed (e.g.for feeding poultry).
                                                                                                                                                                                             12.2%; Score 222.5; DB 1
33.1%; Pred. No. 1.3e-10;
                                                                                                                                                                                                                                                         25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "signal peptide"
30..246
/note= "mature lichenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 24-25; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW37884 standard; Protein; 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0027882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fermentation processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li X, Ljungdahl
                                                                                                                                                                                                                                                            57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-240094/21.
N-PSDB; AAV29067.
                                                                                                                                                                                                                              Similarity
                                                                                                                              237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lichenase protein.
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The corresp. gene and the plant promoter region are inserted into an expression vector and used to transform barley cells. The transformants are used to regenerate barley plants which are useful in brewing. This
                                                                                                                                                                                                                                                                                                                                                                                 EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                               23 TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 RKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by transforming cells with appropriate vector then regeneration giving seeds useful in brewing without conversion to malt.
                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prepn. of barley plants expressing heat stable beta-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 234;
                                                                              Thermostable beta-glucanase production - using Bacillus subtilis transformed with gene from Bacillus
                                                                                                                                                                                                                                                                                                                                74; Indels
                                                                                                                                                                               The gene encoding Bacillus macerans thermostable beta-glucanase is expressed in Bacillus subtilis. The enzyme is useful for lowering the viscosity of brewing mashes and in the production of feedstuff.
                                                                                                                                                                                                                                                                                              Score 228; DB 11;
Pred. No. 4.3e-11;
5; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endo-beta-1,3-1,4-glucanase; barley; brewing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baumlein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR05803 standard; protein; 237 AA
                                                                                                                                                                                                                                                                           12.5%; Scor-
34.3%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mendel R-R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88DD-0320082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; ; p; German.
                                                                                                                                                Fig 1; ; 9pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wobus U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1990-210631/28.
                              WPI; 1990-067913/10.
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                 234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus macerans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ05167.
                                                 N-PSDB; AAQ03519
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                                                                                                                                                                                                                                                                                                                                90;
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 Borriss R;
                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR05803;
                                                                                                                 macerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                129
                                                                                                                                                                                                                                                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>ئ</u>
                                                                                                                                                                                                                                                                                                            Producing nucleic acid encoding lichenase, useful for producing enzymes for improving filtration in brewing, comprises isolating the nucleic acid from soil bacteria
Soil bacterium; enzyme; lichenase; endo-1,3/1,4-beta-glucanase; brewing
                                                                                                                                                                                                                                                                                                                                                                                                                 an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 TSPSYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a protein sequence from a soil bacterium for enzyme with lichenase/endo-1,371,4 beta-qlucansee (E.C. 3.2.1.73) activity. The enzyme is useful in brewing and for degrading beta-glucanases that cause problems during filtration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.6%; Score 229; DB 23; Length 214; 36.1%; Pred. No. 3.2e-11; live 22; Mismatches 67; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermostable beta-glucanase; ss; Bacillus subtilis.
                                                                                                                                                                                            (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKTEGGOVSNLTGTQGLRFNLWSSESA-AWVGQFD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 18; Page 21-22; 27pp; Spanish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR03775 standard; protein; 234 AA
                                                                                                                                                                                                                               Rodriguez Munoz V, Perez Mellado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DEAK ) AKAD WISSENSCHAFT DDR
                                                                                                                             27-JUL-2001; 2001WO-ES00303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermostable beta-qlucanase
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                                                                                                                                                             28-JUL-2000; 2000ES-0001922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 36.1
nes 56; Conservative
                                                                                                                                                                                                                                                          WPI; 2002-217195/27.
N-PSDB; ABL53375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus macerans
                                                             WO200212511-A1
                              Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JUL-1990
                                                                                              14-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Query Match

Best Loc Matches

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117

83

173

RESULT 7 **AAR03775** 

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190
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ABB76859
                               RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 INVSAKDFSGAELYILEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                Vonwettstein D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This hybrid protein is encoded by the beta-glucanase-Hi gene. Following processing of the signal peptide the mature protein is produced, comprising the amino termina of the amylolique faciens beta-glucanase and the carboxyl-terminal half of the B.macerans beta-glucanase. This hybrid protein is thermostable and hydrolyses beta-glycosidic linkages in (1,3-1,4)-beta-glucans. Reducing sugars are obtd. at high temps. and thus this enzyme can be used in the mfr. of food prods., esp. beer and animal feed (eg for feeding poultry). See also AAQ05833.
            RKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 195
                                                                                                                                                                                                                                                                                                                                                                                                                              New thermostable (1,3-1,4)-beta-glucanase - prepd. using hybrid gene obtd. using Bacillus amyloliquefaciens and B.macerans genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 195
                                                                                                                                                                                                       1..129
/label-amino terminal of beta-amyloliquefaciens
133..236
                                                                                                                                                    pre-beta-glucanase; glucans; beer; animal feed; poultry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                          133..236
/label=carboxyl-terminal of B.macerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70;
                                                                                                                                                                                                                                                                                                                                                                                Olsen O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.6%; Score 248; DB 11;
35.4%; Pred. No. 9.3e-13;
1ve 27; Mismatches 70;
                                                                                                                                                                       Bacillus amyloliquefaciens, Bacillus macerans.
                                                                                                                                                                                                                                                                                                                                                                               Thomsen KK,
                                                                                                                                Hybrid (1,3-1,4)-pre-beta-glucanase
                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; page 26; 84pp; English.
                                                                      Ā
                                                                    AAR06621 standard; protein; 239
                                                                                                                                                                                                                                                                                                                                                (CARL-) CARLSBERG A/S.
(DEAK ) AKAD WISSENSCHAFT DDR.
                                                                                                                                                                                                                                                                                               90WO-DK00044.
                                                                                                                                                                                                                                                                                                                   89DK-0003848.
89DD-0325800.
                                                                                                                                                                                                                                                                                                                                                                              Borriss R, Hofemeister J,
                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 35.4
nes 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1990-275129/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ05832
                                                                                                                                                                                                                                                                                                                   04-AUG-1989;
16-FEB-1989;
                                                                                                                                                                                                                                                                                              16-FEB-1990;
                                                                                                             09-JAN-1991
                                                                                                                                                                                                                                                       WO9009436-A
                                                                                                                                                                                                                                                                          23-AUG-1990
                                                                                       AAR06621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
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                                                                                                                                                   Hybrid
                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                          Domain
143
                   165
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                                                           AAR06621
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Soil bacterium; enzyme; lichenase; endo-1,3/1,4-beta-glucanase; brewing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing nucleic acid encoding lichenase, useful for producing enzymes for improving filtration in brewing, comprises isolating the nucleic acid from soil bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a protein sequence from a soil bacterium enzyme with lichenase/endo-1,3/1,4-beta-glucanase (E.C. 3.2.1.73) activity. The enzyme is useful in brewing and for degrading beta-glucanases that cause problems during filtration.
                    237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 229; DB 23;
Pred. No. 3e-11;
2; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 18; Page 18-19; 27pp; Spanish.
                                                                                                                                  Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB76859 standard; Protein; 214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rodriguez Munoz V, Perez Mellado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.6%; Scor
36.1%; Prec
                                                                                                                                ABB76858 standard; Protein; 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JUL-2001; 2001WO-ES00303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-2000; 2000ES-0001922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                             Bacterial lichenase #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacterial lichenase #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-217195/27.
N-PSDB; ABL53374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                WO200212511-A1.
                                                                                                                                                                                                                                                                                                                                                    Unidentified.
                                                                                                                                                                                                                    27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                           14-FEB-2002.
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2000US-0181473.
2000US-0247126.
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                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-497082/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Von Wettstein D,
                                                                                                                                                                                                                                                                                                                     Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                           WO200159141-A2.
                                                                                                                                                                                                                             06-NOV-2001
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09-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                      16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62;
                                                                                                                                                                                                   AAE07317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                           137
                                                                                    143
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                                                                                                                                                  9
                               This sequence represents a novel beta-glucanase isolated from Bacillus alkalophilus DSM 9956. This enzyme is useful for removing glucan and/or lichenan from membranes and equipment in the food industry, especially the brewing industry.
                                                                                                                                                                                        89 PGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGG 148
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                        29 DFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKN 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The lichenase gene from Bacillus subtilis Y-25 is used for transforming Bacillus hosts so that they show increased lichenase expression. The recombinant lichenase enzyme produced by the transformants is useful in beer production for decomposing beta-
                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fermentation; barley; beta-glucan; hydrolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant plasmid used in beer prodn. - obtd. by integrating lichenase gene derived from Bacillus subtilis, into vector
                                                                                                                        Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 242;
                                                                                                                                                                                                                                                                            149 QVSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP 196
                                                                                                                                                                                                                                                                                              209 -TENIPQTPQKIMMNLWPGIGVDGWTGVFDGEDTPVVTEYDWV---RYTP 254
                                                                                                                                                  Indels
                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.7%; Score 250.5; DB 10; 35.5%; Pred. No. 5.8e-13; ... wtematches 75;
                                                                                                                      14.1%; Score 257.5; DB 20; 36.5%; Pred. No. 2.1e-13; ive 22; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                   AAP95000 standard; Protein; 242 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 4; 7pp; Japanese
          Claim 6; Page 5; 8pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus subtilis lichenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87JP-0224615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87JP-0224615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ASAK ) ASAHI BREWERIES KK.
                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                    Similarity 36.5
52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis Y-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1989-119863/16.
N-PSDB; AAN95000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glucan from barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 AA;
                                                                                               308 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP01067181-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                    12-FEB-1997
                                                                                                                                               62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lichenase.
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                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                          AAP95000;
                                                                                                                        Query Match
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Matches
                                                                                                                                                                                                 96
                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                          RESULT 2
AAP95000
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The present invention relates to a food stuff comprising barley feed and transgenic barley malt where the transgenic barley malt comprises a recombinant carbohydrate degrading enzyme comprising a (1,3-1,4)-beta-glucanase. The food stuff is useful to feed animal, preferably chickens Barley is cheaper than corn, the principal foodstuff of chickens. Chickens cannot efficiently utilise barley as an energy source as they do not possess a gut enzyme that depolymerises beta-D-glucan, major carbohydrate present in the barley endosperm. The invention provides a barley based foodstuff which comprises a recombinant carbohydrate degrading enzyme improving the nutritional value of the foodstuff.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barley; transgenic barley malt; carbohydrate degrading enzyme; chicken; (1,3-1,4)-beta-glucanase; nutritional value; foodstuff; thermostable.
                                         52 ISPSYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New barley based foodstuff for animals, i.e. chicken comprising recombinant carbohydrate degrading enzyme (1,3-1,4)-beta-glucanase
EVLGKNPGSFQSNIITGKACAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barley recombinant, thermostable (1,3-1,4)-beta-glucanase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                               RKTEGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 193
                                                                                                                                                                               Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.6%; Score 24%; L. 35.4%; Pred. No. 8e-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UNIW ) UNIV WASHINGTON STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 37-38; 43pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1,3-1,4)-beta-glucanase enzyme.
                                                                                                                                                                                                                                                                                                                                                              AAE07317 standard; Protein; 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
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Gaps

11;

Indels

23 TNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDI 82

61; Conservative

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January 9, 2003, 12:05:57; Search time 36.3542 Seconds (without alignments) 1279.206 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SIDS2/gcgdata/geneseq/geneseqp-embl/AA198. DAT:*
5 ISDS2/gcgdata/geneseqy-embl/AA198. DAT:*
5 ISDS2/gcgdata/geneseqy-embl/AA198. DAT:*
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                                                                                                                                                                                                                                                                                                                                                                            1 MNIKKTAVKSALAVAAAAAA......AKGAKVNPNGHKRYRVNFEH 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1824
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Match
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222.5
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                                                                                                                                                                                         Run on:
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No
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Hillen W, Maurer K; (HENK ) HENKEL KGAA. 30-JUL-1997; 30-JUL-1997; B. alkalophilus be Bacillus subtilis Barley recombinant Hybrid (1,3-1,4)-p Bacterial lichenas Bacterial lichenas Thermostable beta-AAW93001 AAP95000 AAE07317 ABB76621 ABB76859 AAR03775 AAR05629

97DE-1032751. 97DE-1032751. New Bacillus alkalophilus beta-glucanase protein and gene - useful for removing glucan and/or lichenan from membranes in the brewing industry

WPI; 1999-122161/11. N-PSDB; AAX02912.

Heat-stable endo-b Hybrid (1,3-1,4)-p Lichenase protein

7	5		282 288 286 286 284	23 23 23 23 23 23 23 23 23 23 23 23 23 2		thall thall acti acti acti acti
4 N 9 C 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	1157.5 1157.5 1157.5 1157.5 1157.5 1156.5 1156.5 1154.5 1154.5 1155.5 1145.5 1145.5 1145.5 1145.5 1145.5	COCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	2699 2699 2699 2699 2699 2699 2699 2699	7 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	AAG20347 AAG20350 AAG52653 ABB93167 AAG20346 AAG20328 AAG20328 AAG20328 AAG20328 AAG93854 AAB93852 AAY0360 ABB93852 AAG40360 ABB90942 AAG40359 AAG40359 AAG40359 AAG40359 AAG40359 AAG40359 AAG40359 AAG40359 AAG40359 AAG40359 AAG40359	Arabidopsis thalia Arabidopsis thalia Clostridium perfri Gerskovia beta-1,3 Protein encoded by A. thaliana merist Herbicidally activ Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia
RESULT 1 AAW93001 XX XX AAC AAW93 XX XX DJ 19-MA XX XX BELA-IX XX DAI	001 s 001; x-199 kalop gluca ment; lus a 32751		ote glu try	ln; 3 /) gluca ; bre	ALIGNMENTS  8 AA.  protein. ; removal: lichenan ing.	; membrane;

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13;
                                                                                                                 64; Gaps
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                                                                                                                                                                                                                                   168 SAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGSDFTLDWTDNFDTFDGSRWGKGDWT 227
                                                                                                                                                                                                                                                                                                                                                                          152 NTHTLGEFQTGEQAELATITFAKAPDLTSNSVNVTGDVAL-----TADGVEVFGGFYT 204
                                                                                                                                                1 MNIKKTAVKSALAVAAAAAALTTNVSAKD----FSGAELYTLEEVQYGKFEARMKMAAAS 56
                                                                                                                                                                     228 FDGNRVDLTDKNIYSRDGMLILALTRKGQESFNGQVPRDDEPAPQSSSSAPASSSS 283
                                                                                                                                                                                                                                                                                                                                                                                                                                   205 AGEELAPIT-INLTADEGC------GSTPEPEDPETPSASSSDVSSS 245
                                                                               Query Match 5.0%; Score 91; DB 9; Length 279; Best Local Similarity 22.6%; Pred. No. 2.2; Matches 67; Conservative 39; Mismatches 126; Indels
; LENGTH: 279
; TYPE: PRT
; ORGANISM: COTYNEbacterium glutamicum
US-09-738-626-3942
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Search completed: January 9, 2003, 12:14:42 Job time: 10.8866 secs

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CURRENT APPLICATION NUMBER: US/09/738,626
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688 LSSLVFTLALNQEALQNLIN 707
                                                                                                                                           NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 6377
LENGTH: 714
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                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 68; Conserv
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US-09-738-626-3942
                                                                                                                                                                                                                   TYPE: PRT
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                             1080 NGSIRSDISYONIDAIVLPTLPKLRHWFMSDRFSEQGDIMAKFQGALNRAYAQLEQNTLL 1139
                                                                                         56 SGTVSSMFLYQNGSEIA----DGRPWVEVD-IEVLGKNPGSFQSNIITGKAGAQKTSEK 109
                                                                                                                                         168 SAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGSDFTLD------WIDNFDTFD 217
                                                                                                                                                                                                               218 GSRWGKGDWTFDGNRVDLTDKNIYSRDGMLI---LALTRKGQESFNGQVPRDDEPAPQSS 274
                                                                  110 HHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSS--E 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 RDDEPAP-----QSSSSAPASSSSVPASSSSVPASSSSAFVPPSSSSATNAIHGMRTTPA 319
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APPLICANT: ROSEN et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SEQ ID NO 1154

LENGTH: 156
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38.0%; Pred. No. 0.7;
iive 14; Mismatches
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATEISHI, NAKNO
APPLICANT: TATEISHI, NAKO
APPLICANT: TATEISHI, NAKO
APPLICANT: TATEISHI, NAKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKENOMAKINI
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1154, Application US/09925301
Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 VAKEHRNLVNAKGAKVNPN 338
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hes 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1154
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1276 ASSTNSDTSM 1285
                                                                                                                                                                                                                                                                                      275 SSAPASSSSV 284
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US-09-738-626-6377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         495 TEFYSSRVNTQYSAVHLGCAGNRPEMKLRQMEMEESMFGD--WHDWGVEVFDCQIVFTID 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             553 GKAVTSSGKDVFGNSVTPAAAPLRPAHFKLSEEEYREVIGQ-----PWHLILNTM---- 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 YTPGQGEGGSDFTLDWTDNFDTFDGSRWGKGDWTFDGNRVDLTDKNIYSRDGMLILALTR 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 KGQESFNGQVPRDDEPAPQSSSAPAS---SSSVPASSSSVPASSSSAFVPPSSSSATNA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :| | :: | |: | |: | |: | | 36 XSSARVH-LPEIPAGNFRLTVRARAQSEELVDGVRPAIWMQNNTNFCADNDGRPYGELDI 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 -EVLGKNPGSFQSNIITGKAG---AQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVD 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQEV----RKTEGGQVSNLTG-TQGLRFNLMSSESAAWVGQFDESKLPLFQFINWVKVYK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 FSCAELYTLEEVQYGKFEARMKMAAAS-----GTVSSMFLYQNGSEIA--DGRPWVEVDI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.1%; Score 93; DB 9; Length 714;
21.2%; Pred. No. 5.4;
tive 48; Mismatches 136; Indels
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GENEKAL INFOURATION:
APPLICANT: NARACAWA, SATOSHI
APPLICANT: MISOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATEISHI, NAKKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAKKO
APPLICANT: TATEISHI, NAKKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, ARI
CURRENT ELING DATE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 1099-12-16
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-4-07
PRIOR FILING DATE: 2000-04-07
SOFTWARE: PALECATION NUMBER: JO 00/280988
CURRENT FILING DATE: 2000-12-18
PRIOR PAPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6377
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212 NFDTFDGSRWGK - - GDWTFDGNRVDLTDK -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 SEDTLDSTPETEQTKSNGNQDGSSETKDTQVSESPESTPSPDDVLGKGGGIYTEKSLTIT 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLTGTQGLRFNLWSSESAAWVGQFDESKLPLFQFINWVKVYKYTPGQGGGGSDFTLDWTD 211
                                                                                                                                                                                                                                                                                                                                            326 GITGTIDFVSNI-ATDSGA--GVFTKENLSCTN-TNSLQFLKNSAGQHGGGAYVTQTMSY 381
                                                                                                                                                                                                                                                                                                                                                                                                  261
                                                                                                                                                                                                                                                                                                                                                                                                                               382 INTISESITIPPLVGEVIFSEN----TAKGHGGGICTNKLSLSNLKTVTLTKNSAKESGG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----QVPRDDEPAPQS-SSSAPASSSSVPAS-----SSSVPASSSSAFVPPSSS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 MFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAF 121
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                                                                                                                     174 NIKSLLVE-----VTEATFSS 210
                                                                                                                                                             MFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAF 121
                                                                                                                                                                                                                                       HTYGLEWTPNYVRWTVDG-----QEVRKTE-----------GG-----QVS 151
                                                                                                                                                                                                                                                                                                                    152 NLTGTQGLRFNLWSSESAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGSDFTLDWTD 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 5.3%; Score 96; DB 10; Length 1776;
Best Local Similarity 21.2%; Pred. No. 10;
Matches 87; Conservative 49; Mismatches 170; Indels 104; Gaps
                                           Gaps
                                                                                2 NIKKTAVKSALAVAAAAAALTTNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSS 61
                                                                                                                                                                                                  ----NGGEQGGGIYSEQDMLISDCNNVHFQGNAAGATAVKQCLDEEMIVLLTECVDSL
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                                                                                                                                                                                                                                                                                                                                                                                                212 NFDTFDGSRWGK--GDWTFDGNRVDLTDK-----NIYSRDGMLILALTRKGQESFNG
                                       49; Mismatches 170; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 179, Application US/09841132
Patent No. US20020061848A1 •
GENERAL INFORMATION:
APPLICANT: Bhatia, Ajay
APPLICANT: Bratia, Ajay
APPLICANT: Brobst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306 SATNAIHGMRTTPAVAKEHRNLVNA------KGAKVNPNGHKRYRVN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOTDOTETSDTNSDIDVSIENILNVAINONTSAKKGGAIYGKKAKLSRIN 544
Length 821;
  DB 10;
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SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 179
LENGTH: 1776
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    5.3%; Score 96; 21.2%; Pred. No.
  Query Match 5.3%
Best Local Similarity 21.2%
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Chlamydia
US-09-841-132-179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-841-132-179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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13;
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- NIYSRDGMLILALTRKGQESFNG
                                     395 TNTTSESITTPPLVGEVIFSEN----TAKGHGGGICTNKLSLSNLKTVTLTKNSAKESGG
                                                                                  262 -----QVPRDDEPAPQS-SSSAPASSSSVPAS-----SSSVPASSSSAFVPPSSS
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                                                                                                                                                                           306 SATNAIHGMRTTPAVAKEHRNLVNA------KGAKVNPNGHKRYRVN 346
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE: E. COli NM522(pMYC 1628) NRRL B-18652
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                                                                                                                                                Schwab, George E.
Schwab, George E.
Payne, Jewel M.
Narva, Kenneth E.
Foncerrada, Luis
TITLE OF INVENTION: Nematicidal Proteins
NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APLICATION NUMBER: 09/076,137
FILING DATE: 12-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-20CCCD3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.2%; Score 95.5; Di 23.6%; Pred. No. 7.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/738,363
FILING DATE: 15-Dec-2000
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: BACILLUS THURINGIENSIS INDIVIDUAL ISOLATE: PS17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1289 amino acids
                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09738363
Patent No. US20010010932A1
GENERAL INFORMATION:
APPLICANT: Schnepf, Harry E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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ORGANISM: Saccharomyces cerevisiae
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Matches 79; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339 LRQSSTVSSTGSKSGP 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Chlamydia
US-09-841-132-195
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                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 MFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAF 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 GITGTIDFVSNI-ATDSGA--GVFTKENLSCTN-TNSLQFLKNSAGQHGGGAYVTQTMSV 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 5.3%; Score 97; DB 10; Length 1770; Best Local Similarity 21.5%; Pred. No. 8.4; Matches 88; Conservative 46; Mismatches 172; Indels 104; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 NIKKTAVKSALAVAAAAALTINVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSS 61
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                                                                                                                                          APPLICANT: Bhatta, Ajay
APPLICANT: Bhatta, Ajay
APPLICANT: Braita, Ajay
APPLICANT: Brobst, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION FILE REFERBNCE: 210121.46968
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEO ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SATNAIHGMRTTPAVAKEHRNLVNA------KGAKVNPNGHKRYRVN 346
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ORGANISM: Chlamydia trachomatis serovar D
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Milne, Todd
No. US20020128250Alman, Thea
Keyer, John
Salama, Sofie
                                                                                        US-09-841-132-444
; Sequence 444, Application US/09841132
; Patent No. US20020061848A1
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Patent No. US20020128250A1
GENERAL INFORMATION:
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APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Hockt, Doug
APPLICANT: Madden, Kevin
|: | :|:
1373 SSTNSDTSM 1381
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LENGTH: 1770
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APPLICANT:
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APPLICANT:
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APPLICANT: SILVA, Jeff
APPLICANT: SLIVA, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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21.0%; Pred. No. 1.8;
tive 49; Mismatches 147; Indels 101;
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Patent No. US20010010932A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NF-----DLTDG--SRWGKGDWTFDGNRV-----DLTDKNIYSRDGMLILA--- 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LTRKGQESF-NGQVPRDDEPAPQ----SSSSAPASSSSVPASSSSVPASS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               630 NPEDWNIPEGLYRNGEFVFKNGARSTWSSPAPQQPPSTESSSSSSDS3TSQSSSTTPSTN 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 LRFNLWSSESAAWVGQFDESKLPLF-----QFINWVKVYKYTPGQGE-GGSDFTLDWTD 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     570 NHIKTSOFVAPDELFAGYTRKYSMAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                          APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 5.8%; Score 106.5; I
Best Local Similarity 23.5%; Pred. No. 0.4;
Matches 76; Conservative 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 GTVSSMFLYQNGSEIADGRPWVEVDIEVLGKN---
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/259,931
PRIOR FILING DATE: 2000-12-26
PRIOR FILING DATE: 2000-12-26
PRIOR FILING DATE: 2001-02-16
NUMBER 05 SEQ ID NOS: 14110
SOFTWARRE: FASLERO FOR WINDOWS VERSION 4.05
                                                                Sequence 13423, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Streptococcus pneumoniae US-09-815-242-13423
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                                                                                                                                                                             APPLICANT: Zyskind, Judith W. APPLICANT: Wall, Daniel APPLICANT: Trawick, John D.
                                                                                                                                                              Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212
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; Sequence 2, Application US/09738363

RESULT 7 US-09-738-363-2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 HHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSESA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 SRWGKGDWTFDGNRVDLTDKNIYSRDGMLI---LALTRKGQESFNGQVPRDDEPAPQSSS 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 AWVGQFDESKLPLFQFINWVKVYKYT-PGQGEGGSDFTLD-------WTDNFDTFDG
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                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPACTION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/738,363
FILING DATE: 15-Dec-2000
CLASSIFICATION CURROWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLONE: E. coli NM522(pMYC 1627) NRRL B-18651
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                              Foncerrada, Luis
TITLE OF INVENTION: Nematicidal Proteins
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSE: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
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Best Local Similarity 23.7%; Pred. No. 5.5;
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ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
INDIVIDUAL ISOLATE: PS17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/076,137
FILING DATE: 12-MAY-1998
ATTORNEY/AGENY INFORMATION:
NAME: Sanders, Jay
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
                                                                                                                                                                                                                                                                                                                                ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1385 amino acids
                                                              Payne, Jewel M.
Narva, Kenneth E.
                    APPLICANT: Schnepf, Harry E. Schwab, George E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
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                                                                                                                                                                                                                                                               CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
GENERAL INFORMATION
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US-09-765-272-2
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156
                                                                               259
                                                                                                                                                                            DWTDNFDTFD------GSRWGKGDWTFDGNRVDLTDKNIYSRDGMLILALTRKGQESFN 260
                                                                                                                                                                                                    --TINPPISEVGTLKTKGSKLVIDHWDASTGTISAVSNN------TKTGQ--YA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 GDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAEGPPAE--FC 138
                                                                                                             QGLR---FNLWSSESAAWVGQFDE----SKLPLFQFINWVKVYKYTPGQGEGGSDFTL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 TYGLEWTPNYVRWTVDGQEVRKTE------GG-----QVSNLTGTQGLRFNL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 WSSESAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGSDFTLDWTDNFDTFDGSRWGK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 -ATDSGA--GVFTKENLSCTN-TNSLQFLKNSAGQHGGGAYVTQTMSVTNTTSESITTPP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 GSEI--ADGRP---WVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GDWTFDGNRVDLTDK-----QVPRD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVGEVIFSEN----TAKGHGGGICTNKLSLSNLKTVTLTKNSAKESGGAIFTDLASIPTT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEPAPQS-SSSAPASSSSVPAS-----SSSVPASSSSAFVPPSSSSATNAIHGMRTT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 VKSALAVAAAAAAITTNVSAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQN 67
                                                                   ---AQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEG----GQVSNLTGT
                                                                                                                                           260 LGLRKPFVKFFDNKNNAINPETDAKAREKLSDIPTSMYVDYVRVWEKSAGN-----
                                                                                                                                                                                                                                      GQVPRDDEPAPQSSSSAPASSSSVPASSSSVPASSSSAFVPPSS----SSATN 309
                                                                                                                                                                                                                                                           | | :::: | :::| | :| GSV------NNASIAQIVTLKANTSYKVSAFGKASSPGTSAYLGISKASN 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOR TREATMENT AND INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 583;
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                                                                                                                                                                                                                                                                                                                                           Sequence 353, Application US/09841132
Patent No. US20020061848A1
GENERAL INFORMATION:
APPLICANT: Bhatia, Ajay
APPLICANT: Preser Application Section 3.0/4.0
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR TILLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFF FILE REFERENCE: 210121.469C8
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastsEQ for Windows Version 3.0/4.0
LENGTH: 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-841-132-353
                                                                                                                                                                                                                                                                                                                                    US-09-841-132-353
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20;
                                                                         APPLICANT: Choi et. al.
TITE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGSFQSNIITGKAGA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 GNITLQYALQQSRNV----PAVET-LNKVGLNRAKTFLNGLGIDYPSIHYSNAIS--SNT 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 QKTSEKHHAVS---PAADQAFHTYGLEWTPNYVRWTV--DGQEVRKTEGGQVSNLTGTQG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRFNLWSSESAAWVGQFDESKLPLF-----QFINWVKVYKYTPGQGE-GGSDFTLDWTD 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               517 NHIKTSOFVAPDELFAGYTRKYSMAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGS 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------LTRKGQESF-NGQVPRDDEPAPQ----SSSSAPASSSSVPASSSSVPASS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NF-----DLTDKNIYSRDGMLILA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 666;
                                                                                                                                                                                                                                                                                                   ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.9%; Score 107.5; DB 10; Best Local Similarity 23.5%; Pred. No. 0.3; Matches 76; Conservative 50; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTVSSMFLYQNGSEIADGRPWVEVDIEVLGKN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/961,083
FILING DATE: CUDKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: US-09-765-272-2
Sequence 2, Application US/09765272
Patent No. US20020061545Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 666 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSAFVPPSSSSATNAIHGMRTTP 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STTTNPNNNTQQS----NTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                      STATE: Maryland
COUNTRY: USA
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Glycolyse hydrolase genes and their use for producing enzymes for the biodegradation of
                                        135 WTVDGQEVRKTEG---GQVSNLTGTQGLR--FNLWSSE----SAAWVGQFDESKLPLFQF 185
                                                                   398 WYVDGEIVGEKDNLYWHRQMNLTLSQGLRAPHTOWKCNQFYPSANKSAEGFPTSMEVDYV 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 VKISNGIAELTMRHNANNTPPDGGTYFTSGIFKSYQKFTYGYFEAKIQGADIGEGVCPSF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 FLYQN-GSEIADGRP-WVEVDIEVL-----GKNPGSFQSNI----ITGKAG----- 102
--YHLPFDPRND--FHTYGVNVTKDKIT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 VKSALAVAAAAAALTTNVSAKD----FSGAELYTLEEVQYGKFEARMKMA-AASGTVSSM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: DENNISON, MESEROLE, SCHEINER & SCHULTZ
STREET: 612 Crystal Square 4, 1745 Jefferson Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                              HENRISSAT, Bernard
YVIN, Jean-Claude
KLOARES, Bernard
KIOARES, Bernard
TITLE OF INVENTION: Glycolyse hydrolase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/988,200
FILING DATE: 19-No. US20020094553A1-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/269,731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.3%; Score 114.5; Dl
20.6%; Pred. No. 0.06;
iive 61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: <Unknown>
PEPERENCE/POCKER NUMBER: <Unknown>
TELECOMMUNICATION IRFORMATION:
TELEPHONE: (703) 412-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: <UNKNOWN>
APPLICATION NUMBER: FR 96 12204
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: IRA SCHULTZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             carrageenans
                                                                                                                                                                                                                                                                                                                                        APPLICANT: BARBEYRON, Tristan
POTIN, Philippe
RICHARD, Christophe
349 HNIVVKNGKPTWMRPGSFPQTNHNG---
                                                                                                                                                                                                                                                        US-09-988-200-8; Sequence 8, Application US/09988200; Patent No. US20020094553A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 545 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 412-
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                     458 RTWVKVGNNNSAPGEGQS 475
                                                                                                                          186 INWVKVYKYTPGQGEGGS 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22202
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: VIRGINIA COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 -EVLGKN-----PGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVR 134
                    --OGLRFNLWSSESAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGSDFT 206
                                                        175 PGTKYLNQQAMGVYISIWDGSSWATQG----GRVP----INW------ASAPFT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: US/09/988,200
FILIG DATE: 19-No. US20020094553A1-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: DENNISON, MESEROLE, SCHEINER & SCHULTZ
STREET: 612 Crystal Square 4, 1745 Jefferson Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 YGKFEARMKMAAASGTVSSMF-LYQ--NGSEIADGR-PWVEVDI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.4%; Score 117; DB 10;
27.3%; Pred. No. 0.044;
Live 23; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 412-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/269,731
FILING DATE: 4Unknown>
APPLICATION NUMBER: FR 96 12204
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: IRA SCHULTZ
                                                                                                     207 LDWTDNFDTFDGSRWGKGDWTFDGNRVDLTDKN 239
                                                                                                                                              -----DFALNGCVVDPNDPN 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-988-200-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                    Sequence 6, Application US/09988200
Patent No. US20020094553A1
GENERAL INFORMATION:
APPLICANT: BARBEYRON, Tristan
POTIN, Philippe
"RICHARD, Christophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 620 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (703) 412-1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: VIRGINIA COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22202
                                                                                                                                              215 ATYQ----
                                                                                                                                                                                                             RESULT 2
US-09-988-200-6
                    157
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 9, 2003, 12:05:16; Search time 8.88657 Seconds (without alignments) 761.932 Million cell updates/sec Run on:

US-09-654-652A-3 1824 1 MNIKKTAVKSALAVAAAAAA......AKGAKVNPNGHKRYRVNFEH 349 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

118974 segs, 19401057 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published\_Applications\_AA:\* Database :

/ cgn2\_6/ptodata/1/pubpaa/USO8\_NBW\_PUB.pep:\*
/ cgn2\_6/ptodata/1/pubpaa/DSO8\_NBW\_PUB.pep:\*
/ cgn2\_6/ptodata/1/pubpaa/NSO6\_NBW\_PUB.pep:\*
/ cgn2\_6/ptodata/1/pubpaa/USO6\_PUBCOMB.pep:\*
/ cgn2\_6/ptodata/1/pubpaa/USO7\_NBW\_PUB.pep:\*
/ cgn2\_6/ptodata/1/pubpaa/USO7\_PUBCOMB.pep:\*
/ cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
/ cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
/ cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
/ cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
/ cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
/ cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\* /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*/cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*/cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ				
Result		Query				
. i	Score	Match	Match Length DB	BB	ID	Description
1	120	9.9	287	10	US-09-734-569-152	Sequence 152, App
7	117	6.4	620	10	US-09-988-200-6	Sequence 6, Appli
3	114.5	6.3	545	10	US-09-988-200-8	Sequence 8, Appli
4	108	5.9	583	10	US-09-841-132-353	Sequence 353, App
S	107.5	5.9	999	10	US-09-765-272-2	Sequence 2, Appli
9.	106.5	5.8	719	10	US-09-815-242-13423	Sequence 13423, A
7	97.5	5.3	1385	10	US-09-738-363-2	
80	97	5.3	1770	10	US-09-841-132-444	Sequence 444, App
6	96.5	5.3	526	10	US-09-801-368-362	Sequence 362, App
10	96	5.3	821	10	US-09-841-132-195	
11	96	5.3	1776	10	US-09-841-132-179	Sequence 179, App
12	95.5	5.5	1289	10	US-09-738-363-4	Sequence 4, Appli
13	93	5.1	156	10	US-09-925-301-1154	Sequence 1154, Ap
14	93	5.1	714	σ	US-09-738-626-6377	Sequence 6377, Ap
15	91	5.0	279	0	US-09-738-626-3942	Sequence 3942, Ap
16	91	5.0	678	10	US-09-801-368-314	Sequence 314, App
17	91	5.0	1751	10	US-09-841-132-445	Sequence 445, App
18	91	5.0	1751	10	US-09-841-132-594	Sequence 594, App
19	90	4.9	674	6	US-10-086-464-14	Sequence 14, Appl

Sequence 6780, App Sequence 34, Appl Sequence 108, Appl Sequence 10036, Appl Sequence 10036, Appl Sequence 394, Appl Sequence 1, Appl Sequence 57, Appl Sequence 57, Appl Sequence 57, Appl Sequence 57, Appl Sequence 17, Appl Sequence 16, Appl Sequence 16, Appl Sequence 47, Appl Sequence 475, Appl Sequence 475, Appl Sequence 475, Appl Sequence 2, Appl Sequence 2, Appl Sequence 21, Appl Sequence 192, App
9 US-09-738-626-6780 10 US-09-745-008-34 11 US-01-052-586-592 12 US-01-052-588-108 13 US-09-815-242-10036 14 US-09-811-32-394 15 US-09-811-32-394 16 US-09-863-5478-1 17 US-09-863-5478-1 18 US-09-863-5478-1 19 US-09-100-912-2 10 US-09-100-912-2 10 US-09-100-912-3 10 US-09-975-326-4 10 US-09-975-326-4 10 US-09-975-326-4 10 US-09-975-326-4 10 US-09-975-326-4 10 US-09-975-326-4 10 US-09-975-326-4 10 US-09-975-326-4 10 US-09-975-326-4 10 US-09-975-326-2 10 US-09-975-326-2 10 US-09-975-326-2 10 US-09-975-326-2 10 US-09-975-326-2 10 US-09-975-326-2 10 US-09-975-326-2 10 US-09-975-326-2 10 US-09-975-326-2
493 9 1162 11 1463 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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88 8 88 88 899 899 899 899 899 899 899
0112847869112848999999999999999999999999999999999

## ALIGNMENTS

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APPLICANT: Duvenig, Elke APPLICANT: Schmidt, Ralf-Michael APPLICANT: Schmidt, Ralf-Michael APPLICANT: Schmidt, Ralf-Michael APPLICANT: Schmidt, Ralf-Michael APPLICANT: Reski, Ralf-Michael APPLICANT: Reski, Ralf-Michael TITLE OF INVENTION: More 1332-99-05
TITLE OF INVENTION: in the synthesis of carbohydrates
FILE REFERENCE: BASF-NAE-1332-99-05
CURRENT APPLICATION NUMBER: US 60/171,101
PRIOR PPLICATION NUMBER: US 60/171,101
PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 181
SOFTHARE: PALENTH VET: 2.1/WordPerfect 6.1
LENGTH: 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 VDGVGGRE-QQMYLGFDPSAD--FHYYRFRWSKDMVVFYVDNKPVR-----VFKNLEGTV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 YGKFEARMKMAA--ASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNPGS---FQSNII 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.6%; Score 120; DB 10; Length 287; Best Local Similarity 23.0%; Pred. No. 0.0089; Matches 49; Conservative 30; Mismatches 70; Indels 64
US-09-734-569-152
Sequence 152. Application US/09734569
Patent No. US20020064816Al
GENERAL INFORMATION:
                                                                                                       APPLICANT: Lerchl, Jens
APPLICANT: Renz, Andreas
APPLICANT: Errhardt, Thomas
APPLICANT: Reindl, Andreas
APPLICANT: Cirpus, Petra
APPLICANT: Bischoff, Friedrich
APPLICANT: Frank, Markus
APPLICANT: Frenk, Markus
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US-09-734-569-152
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TYPE: PRT
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17;
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Best Local Similarity 21.9%; Pred. No. 20;
Matches 70; Conservative 36; Mismatches 100; Indels 114; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 WIDNFDIFDGSRWGKGDWIFDGNRVDLTDKNIYSRDGMLILALIRKGQESFNGQ----V 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 MAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHH 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 PRDDEPAPQSSS-SAPASSSSV---PA--SSSSVPASSSSAFVPPSSSSATNAIHGMRTT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| | | : | : | : | | | : | 1383 WKDYFPEPVIVSMSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNVNHK 242
                                                                                                                                                                                                                                                                                                                                                                           112 AVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSESAAW 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 VGQFDESKLPLFQFINWVKVYK----YTPGQGEG-------GSDFTLD 208
                                                                                                                                                                                                                                                                                                                            47 ----ASGGTFSMYGFNW------VRQAPG------HGIE------W 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: January 9, 2003, 12:14:20 Job time : 22.3495 secs
PRIOR APPLICATION NUMBER: 60/329,709
PRIOR FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 3
LENGTH: 261
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 PSNTKVDK-----KVEP 254
                                                                                                                                                     FEATURE:
CTHER INFORMATION: Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 LYTLEEVQY-GKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQ 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1602;
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GENERAL INFORMATION:
APPLICANT: COMPUGEN LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 83342
                                                                                                                                      Variants of alternative splicing
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19.0%; Pred. No. 1.4e+02;
tive 45; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.4%; Score 98.5; DB 5; 19.5%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 TGT-----QGL-----RFNLWSSESAAWVG-----
                  Sequence 83344, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNDRER: US/09/724,676A
CURRENT APPLICATION UNDRES: 009/11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
LENGTH: 1602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-83344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-83342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 51; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 60; Conserva
US-09-724-676A-83344
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US-09-724-676-83342
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE SECRETAR
APPLICANT: DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
TITLE OF INVENTION: IMMUNOBELICIENCY VIRUS SELECTED BY ENV-CD4-CO-RECEPTOR COMPLE
FILE REFERENCE: 218837
CURRENT APPLICATION NUMBER: PCT/US02/33165
CURRENT FILING DATE: 2002-10-16
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1315 HGLLKTEAESYEGLLGERLRERGGEESKEECVWVGGHKGAWGWGGTFGYSCGPCLVLSPA 1374
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GENERAL INFORMATION:
TITLE OF INVENTION: Variants of alternative splicing
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 83342
LENGTH: 1629
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Best Local Similarity 19.0%; Pred. No. 1.4e+02;
Matches 60; Conservative 45; Mismatches 108;
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US-09-724-676A-83342
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US-09-724-676A-83343
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TQGLRFNLWSSESAAWVGQFDESKLP-LFQFINWVKVYKYTPGQGE-
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT APPLICATION NUMBER: US/09/724,676A
SOFTWARE OF SEQ. ID NOS: 97222
SOFTWARE Patentin version 3.2
SEQ. ID NO 83343
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18.7%; Pred. No. 1.2e+02;
Live 38; Mismatches 100
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spl:
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724.676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 83343
LENGTH: 1558
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ORGANISM: Homo sapiens
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US-09-724-676-83343
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Matches 59; Conserva
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US-09-724-676A-83343
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US-09-724-676-83343
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GENERAL INFORMATION:
APPLICAMT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 1291814. Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 83344
    ; Score 99; DB 5; Le
; Pred. No. 1.2e+02;
38; Mismatches 100;
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; Pred. No. 1.4e+02;
33; Mismatches 85;
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Best Local Similarity 19.5%
Matches 51; Conservative
                                                Conservative
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CRGANISM: Homo sapiens
US-09-724-676-83344
Query Match
Best Local Similarity
Matches 59; Conserv
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US-09-724-676-83344
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US-09-724-676A-83341
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                                                                                                                                                                                  493 GASVNTVEEAGAYGAF-----ANGCTYYKPY-YVNKVVSADGNTQTFNSQGTRAMKSS
                                                                                                                                                                                                                                                                                                               597 IAKDAWFTGYTRNRVISVWT--GYDKPTSHGISYAEQTISQ------
                                                                                                                                                                                                                                                                                                                                                   177 ESKLPLFQFINWVKVYK----YTPGQGEGGSDFTL-DWTDNFDTFDGSRWGKGDWTFDGN
                                                                               Query Match 5.7%; Score 103.5; DB 6; Length 771; Best Local Similarity 22.7%; Pred. No. 28; Matches 79; Conservative 37; Mismatches 117; Indels 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 PASSSSAFVPPSSSSATNAIHGMRTTPAVAKEHRNLVNAKGAKVNPNG 339
                                                                                                                                                   32 GAELYTLEEV-QYGKFEARMKMAAASGTVSSMFLYQNGSEIADGR----
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GENERAL INFORMATION:
FAPLICANT: Compagen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compagen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
LENGTH: 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 KVYKYTPGQ------GEGGSDFTLDWTDNFDTFDGSRWG 222
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20.8%; Pred. No. 61;
tive 36; Mismatches
               TYPE: PRT ORGANISM: Lactobacillus rhamnosus
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US-09-724-676-83341
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US-09-724-676-83341
                                  ; ORGANISM: Lac
US-10-264-213-165
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LENGTH: 771
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Best Local (
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RESULT 7

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APPLICANT: FORSYLM, R. Allyn
APPLICANT: FORSYLM, R. Allyn
APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Kari
APPLICANT: Zyskind, Judih
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THER
FILE REFERENCE: ELITRA.008DV1
CURRENT APPLICATION NUMBER: US/10/287,274
CURRENT FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 2000-11-09
NUMBER OF SED ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 406
LENGTH: 571
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 83341
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.7%; Score 103.5; Best Local Similarity 20.8%; Pred. No. 61; Matches 46; Conservative 36; Mismatches
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Sequence 83341, Application US/09724676A GENERAL INFORMATION:
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US-10-287-274-406
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US-09-724-676A-83341
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                                                                                                                                                                                Sequence 137, Application US/10264213 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79; Conservative
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Best Local Similarity
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US-10-264-213-165
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| 315 HG------LKTEAESYEGLLAPSLIPKNWPDQGKIQIQNLSVRYDSSLKPVLKHVNAL 1367
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 83340
                  TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION NUMBER: US/09/724,676 CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222 SOFTWARE: Patentin version 3.2 SOFTWARE:
                                                                                                                                                                                                                                                               DB 5;
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                                                                                                                                                                                                                                                          5.7%; Score 104; DB : 19.7%; Pred. No. 55; tive 41; Mismatches
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19.7%; Pred. No. 5
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US-09-724-676A-83340
; Sequence 83340, Application US/09724676A
; GENERAL INFORMATION:
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Best Local Similarity 19.7%
Matches 54; Conservative
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Matches 54; Conservative
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; ORGANISM: Homo sapiens
US-09-724-676-83340
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; ORGANISM: Homo sapiens
US-09-724-676A-83340
APPLICANT: Compugen LTD
                                                                                                                                                             LENGTH: 1510
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76 -PWVEVDI--EVLGKNPGS-----FQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYG 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 115;
                                                                                                                                                                                                                             APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Havukkala, Ilkka J
APPLICANT: Lavukkala, Ilkka J
APPLICANT: Lavukkala, Ilkka J
APPLICANT: Lavukkala, Ilkka J
TITLE OF INVENTION: Polyuucleotides, materials incorporating
TITLE OF INVENTION: them, and methods for using them.
FILE REFERENCE: 11000-1043 cd 3400/264,213
CURRENT APPLICATION NUMBER: US/10/264,213
CURRENT FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 137
LENGTH: 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 165, Application US/10264213
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Glann, Matthew
APPLICANT: Lubbers, Mark William
APPLICANT: Dekker, James
TITLE OF INVENTION: them, and methods for using them.
FILE REFERENCE: 11000.1043 c3
CURRENT APPLICATION UNMBER: US/10/264,213
CURRENT FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 253
SOGTWARE: FeastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 771;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 GAELYTLEEV-QYGKFEARMKMAAASGTVSSMFLYQNGSEIADGR-----
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1424 FVRKTSIFIMDEATASIDMATENILQKVVMTAFA 1457
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18;

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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	Copyright (c) 1993 - 2003 Compugen Ltd.
OM protein - pr	OM protein - protein search, using sw model
Run on:	January 9, 2003, 12:04:12 ; Search time 15:3495 Seconds (without alignments) 1613.076 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-654-652A-3 1824 1 MNIKKTAVKSALAVAAAAAAAKGAKVNPNGHKRYRVNFEH 349
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	263044 seqs, 70945482 residues

Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending\_Patents\_AA\_New:\*

1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep:\*
7: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 3, Appli			137,	165,	8334		406,	Sequence 83343, A		83344,	Sequence 83344, A	83342,		'n	88017,	88017,	88018,	Sequence 88018, A	88014,	88014,	Sequence 88015, A	88015,		Sequence 88016, A	Seguence 88013, A
ID	US-10-294-561-3	-09-724-	-09-724-676A-8	-10-264-213-13	-264-	-09-724-	-60-	-10-287-	724-	19-724-	US-09-724-676-83344	9-724-	24	US-09-724-676A-83342	r-us02-	-09-724		-09-724	-09-724-	-09-724-	US-09-724-676A-88014	US-09-724-676-88015	US-09-724-676A-88015	-724-	-09-724-	US-09-724-676-88013
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Score	116.5	104	104	103.5	103.5	103.5	103.5	66	66	66	8	98.5	æ	8	86	98	98	98	86	98	86	86	98	98	86	96
Result No.		7	e	4	5	9			6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56

Sequence 88013, A Sequence 6133, Ap		Sequence 1484, Ap	٠.	Sequence 53372, A		Sequence 53372, A		Sequence 32, Appl	Sequence 2398, Ap	Sequence 56516, A		592,	Sequence 592, App	Sequence 592, App	Sequence 592, App	Sequence 56515, A	Sequence 56515, A
US-09-724-676A-88013 US-09-134-000C-6133	PCT-US02-33165-11	US-10-276-774-1484	US-09-724-676-53371	US-09-724-676-53372	US-09-724-676A-53371	US-09-724-676A-53372	US-09-917-384A-1	US-10-171-404A-32	US-10-276-774-2398	US-09-724-676-56516	US-09-724-676A-56516	US-10-125-923A-592	US-10-205-892-592	US-10-174-575-592	US-10-174-575A-592	US-09-724-676-56515	US-09-724-676A-56515
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86 96	94	91	91	91	91	91	91	90.5	90.5	88	88	83	89	89	88	89	89
27 28	29	30	31	32	33	34	35	36	37	. 38	39	40	41	42	43	44	45

## ALIGNMENTS

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAMY: Salkagava.
TITLE OF INVENTION: (1-3)-Beta-D-Glucan Binding Domain Protein, Measuring Method U
TITLE OF INVENTION: (20218
TITLE OF INVENTION: Substance And Assay Kit
FILE REPRENCE: 022918
CURRENT APPLICATION NUMBER: US/10/294,561
CURRENT FILING DATE: 2002-11-15
PRIOR RAPLICATION NUMBER: JP 2001-351943
FRIOR RELIGING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 5
SOCTHARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ----WMSGDNTNYVRWPSSGEIDFIEHRNTNNEKVRGTIHWSTPDGAHAHHNRESNTNGI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 -FHTYGLEWIPNYVRWIVDGQEV--RKTEGGQVSNLTGTQGLRFNLWSSESAA----WVG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 : | :| :| :| :| :| 290
233 -FDVADEAFPAKMYIDYVRVYQDASTSSPVGDTSLDGYYFVQNRHSELYLDVTDASNE-D 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 QFD--ESKLPLFQFINWVKVYKYTPGQGEGG-----SDFTLDWTDNFDTFD 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 LTINVSAKDFSGAELYTLEEV-----QYGKFEARMKMAAASGTVSSMFLYQNGSEIA 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        97;
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6.4%; Score 116.5; I
Best Local Similarity 22.3%; Pred. No. 3.3;
Matches 60; Conservative 41; Mismatches
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                                                                                                                                                                                                                                                                                                                                   ORGANISM: Tachypleus tridentatus US-10-294-561-3
                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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RESULT 2
US-09-724-676-83340
Sequence 8340, Application US/09724676
GENERAL INFORMATION:

Search completed: January 9, 2003, 12:13:26 Job time: 118.824 secs

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APPLICANT: Blonomix, Inc.
APPLICANT: Blonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFRENCE: 261,210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 79889
                                                                                                                             APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY P
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 TKVQFNYYTNGAG---NHEKIVDLGFDAANAYHTYAFDWQPNSIKWYVDGQ-LKHTATNQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
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18.4%; Score 245.5; DB 21; Length
Best Local Similarity 35.8%; Pred. No. 1.5e-16;
Matches 59; Conservative 24; Mismatches 71; Indels
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35.8%; Pred. No. 1.5e-16;
iive 24; Mismatches 71
                                              Sequence 73450 Application US/09791537 GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 79889, Application US/09791537 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Bacillus subtilis
US-09-791-537-73450
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; ORGANISM: Bacillus subtilis
US-09-791-537-79889
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                     SEQ ID NO 73450
LENGTH: 242
                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                             APPLICANT: Debb. Derek
APPLICANT: Danzer. Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION UNMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 31771
LENGTH: 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
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                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 VSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP 173
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illarity 35.5%; Pred. No. 1.2e-16;
Conservative 24; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
18.6%; Score 247.5; DB 21;
Best Local Similarity 36.1%; Pred. No. 1.1e-16;
Matches 61; Conservative 20; Mismatches 75;
                 Sequence 31771, Application US/09791537 GENERAL INFORMATION: APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Bacillus subtilis
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US-09-791-537-31771
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60; Conserv
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US-09-791-537-27063
US-09-791-537-31771
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Matches 6
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Search completed: January 9, 2003, 12:14:40 Job time: 7.79861 secs

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B. alkalophilus be
Bacillus subtilis
Barley recombinant
Hybrid (1.3-1,4)-p
Thermostable beta-
                                                                                                                                9, 2003, 12:05:57; Search time 27.8125 Seconds (without alignments) 1279.206 Million cell updates/sec
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                                                                                                                                                                                                                                                    1439
1 MVSAKDFSGAELYTLEEVQY.......PNSSSVDKLAAALEHHHHH 267
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                           908470 seqs, 133250620 residues
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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	ALIGNMENTS					
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Arabidopsis thalia	AAG40361	21	0 -			44
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a-1,3-glucanas	159	12	9		14	42
a xanthin	345	18	3		4	41
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	34	21	9	0	50.	30
~	316	23	9	0	50.	29
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. Clostridium perfri	306	22	4	0	15	25
ro	385	23	8	0		24
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s thali	246	21	8	2	7	13
··	373	23	o		œ	12
thali	346	21	α	2	$\alpha$	11

Beta-glucanase; enzyme; glucan; removal; lichenan; membrane; equipment; food industry; brewing. B. alkalophilus beta-glucanase protein. AA. AAW93001 standard; Protein; 308 97DE-1032751. 97DE-1032751 19-MAY-1999 (first entry) Bacillus alkalophilus Hillen W, Maurer K; WPI; 1999-122161/11. N-PSDB; AAX02912. (HENK ) HENKEL KGAA DE19732751-A1 30-JUL-1997; 30-JUL-1997; 04-FEB-1999. AAW93001; 

New Bacillus alkalophilus beta-glucanase protein and gene - useful for removing glucan and/or lichenan from membranes in the brewing industry

Heat-stable endo-b Bacterial lichenas Bacterial lichenas Hybrid (1,3-1,4)-p Lichenase protein.

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Barley; transgenic barley malt; carbohydrate degrading enzyme; chicken; (1,3-1,4)-beta-glucanase; nutritional value; foodstuff; thermostable.
GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT
                                                                                                                                                                                                                                Barley recombinant, thermostable (1,3-1,4)-beta-glucanase enzyme.
                                                                               EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                                                                           AAE07317 standard; Protein; 214
                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-497082/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 AA;
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                                                                                                                                                                                                                                                                                        Hordeum vulgare.
                                                                                                                                                                                                                                                                                                              WO200159141-A2.
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                                                                                                                                                                                   AAE07317;
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Best Local 3
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                               This sequence represents a novel beta-glucanase isolated from Bacillus alkalophilus DSM 9956. This enzyme is useful for removing glucan and/or lichenan from membranes and equipment in the food industry, especially
                                                                                                                                                                                                                       PGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGG 125
                                                                                                                                       Gaps
                                                                                                                                                           DFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The lichenase gene from Bacillus subtilis Y-25 is used for transforming Bacillus hosts so that they show increased lichenase expression. The recombinant lichenase enzyme produced by the transformants is useful in beer production for decomposing betaglucan from barley.
                                                                                                                                                                                                                                                                                                                                                                                                                             production; fermentation; barley; beta-glucan; hydrolysis;
                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant plasmid used in beer prodn. - obtd. by integrating lichenase gene derived from Bacillus subtilis, into vector
                                                                                                               Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 242;
                                                                                                                                                                                                                                                    126 QVSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP 173
                                                                                                                                                                                                                                                                    - TENIPQTPQKIMMNLWPGIGVDGWTGVFDGEDTPVVTEYDWV---RYTP 254
                                                                                                                                       Indels
                                                                                                                DB 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 246.5; DB 10;
; Pred. No. 1.2e-15;
24; Mismatches 74;
                                                                                                              Score 257.5; DB 2
Pred. No. 1.4e-16;
                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                   AAP95000 standard; Protein; 242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 4; 7pp; Japanese.
                                                                                                              17.9%; Sco
36.5%; Pre
tive 22;
        Claim 6; Page 5; 8pp; German.
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al Similarity 35.5%;
60; Conservative 2.
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                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                              Query Match 17.9
Best Local Similarity 36.5
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus subtilis Y-25
                                                                 the brewing industry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1989-119863/16.
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                                                                                         308 AA
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The present invention relates to a food stuff comprising barley feed and transgenic barley malt where the transgenic barley malt comprises a recombinant carbohydrate degrading enzyme comprising a (1,31,4)-beta glucanase. The food stuff is useful to feed animal, preferably chickens Barley is cheaper than corn, the principal foodstuff of chickens. Chickens cannot efficiently utilise barley as an energy source as they do not possess a gut enzyme that depolymentises beta-D-glucan, major carbohydrate present in the barley endosperm. The invention provides a barley based foodstuff which comprises a recombinant carbohydrate present in the barley endosperm. The invention provides a degrading enzyme improving the nutritional value of the foodstuff. The present sequence is barley recombinant, thermostable (1,3-1,4)-beta-glucanase enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                     New barley based foodstuff for animals, i.e. chicken comprising recombinant carbohydrate degrading enzyme (1,3-1,4)-beta-glucanase
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35.5%; Pred. No. 1.7e-15;
live 26; Mismatches 69;
                                                                                                                                                                               (UNIW ) UNIV WASHINGTON STATE RES FOUND.
                                                                                                                                                                                                                                                      Huang J, Horvath H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 37-38; 43pp; English
09-FEB-2001; 2001WO-US04222.
                                                                      2000US-0181473.
                                                                                                    09-NOV-2000; 2000US-0247126
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3 SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62

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67 GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermostable beta-glucanase production - using Bacillus subtilis transformed with gene from Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 VSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The gene encoding Bacillus macerans thermostable beta-glucanase is expressed in Bacillus subtilis. The enzyme is useful for lowering the viscosity of brewing mashes and in the production of feedstuff.
                                                                                                                                                                                                                                                                                                                                                                             Thermostable beta-glucanase; ss; Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.7%; Score 226; DB 11; 35.1%; Pred. No. 1.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat-stable endo-beta-1,3-1,4-glucanase.
                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                                               234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DEAK ) AKAD WISSENSCHAFT DDR.
                                                                                                                                                      AAR03775 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88DD-0315706.
                                                                                                                                                                                                                                                                                                                        Thermostable beta-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-NOV-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig 1; ; 9pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1990-067913/10.
N-PSDB; AAQ03519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus macerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAY-1988;
                                                                                                                                                                                                                                                                   31-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAY-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DD272102-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borriss R;
                                                                                                                                                                                                                 AAR03775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR05803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      macerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                         193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                          RESULT 5
AAR03775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR05803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This hybrid protein is encoded by the beta-glucanase-H1 gene. Following processing of the signal peptide the mature protein is produced, comprising the amino terminus of the amylolique-faciens beta-glucanase and the carboxyl-terminal half of the B.macerans beta-glucanase. This hybrid protein is thermostable and hydrolyses beta-glucanase. This hybrid protein is thermostable Reducing sugars are obtd. at high temps. and thus this enzyme can be used in the mfr. of food prods., esp. beer and animal feed (eg for feeding poultry). See also AAQ05833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New thermostable (1,3-1,4)-beta-glucanase - prepd. using hybrid gene obtd. using Bacillus amyloliquefaciens and B.macerans genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vonwettstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..129 ....../label=amino terminal of beta-amyloliquefaciens 133..236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                          pre-beta-glucanase; glucans; beer; animal feed; poultry.
                                                     EGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 EGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 17.0%; Score 244; DB 11; Length 239; Best Local Similarity 35.5%; Pred. No. 2e-15; Matches 61; Conservative 26; Mismatches 69; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=carboxyl-terminal of B.macerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olsen O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus amyloliquefaciens, Bacillus macerans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thomsen KK,
                                                                                                                                                                                                                                                                                                                                                                        Hybrid (1,3-1,4)-pre-beta-glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; page 26; 84pp; English.
                                                                                                                                                                                                              AA.
                                                                                                                                                                                                           AAR06621 standard; protein; 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CARL-) CARLSBERG A/S.
(DEAK ) AKAD WISSENSCHAFT DDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90WO-DK00044
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89DD-0325800
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                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1990-275129/36.
N-PSDB; AAQ05832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-AUG-1989;
16-FEB-1989;
                                                                                                                                                                                                                                                                                                                   09-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9009436-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borriss R,
                                                                                                                                                                                                                                                                AAR06621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                             Hybrid
                                                                        168
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Soil bacterium; enzyme; lichenase; endo-1,3/1,4-beta-glucanase; brewing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a protein sequence from a soll bacterium for an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 SYNKFOCGENRSVQTYGYGLXEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDIEFL 114
                                                                                                                            Producing nucleic acid encoding lichenase, useful for producing enzymer for improving filtration in brewing, comprises isolating the nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                              SAKDFSCAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62
                                                                                                                                                                                                                                        The present sequence is a protein sequence from a soil bacterium enzyme with lichensex/endo-1,3/1,4-betts-glucanase (E.C. 3.2.1.73) activity. The enzyme is useful in brewing and for degrading beta-glucanases that cause problems during filtration.
                                                                                                                                                                                                                                                                                                                                                                         Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
 (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
                                                                                                                                                                                                                                                                                                                                                                     15.6%; Score 225; DB 23; 36.2%; Pred. No. 1.2e-13; ive 21; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 ATTQIPAAPGK--IMMNLWNGTGVDDWLGSYN 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFD 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                       Claim 18; Page 18-19; 27pp; Spanish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 18; Page 21-22; 27pp; Spanish.
                                      Perez Mellado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rodriguez Munoz V, Perez Mellado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB76859 standard; Protein; 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JUL-2001; 2001WO-ES00303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-2000; 2000ES-0001922
                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 36.29
Matches 55; Conservative
                                                                                                                                                  for improving filtratior
acid from soil bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-217195/27.
N-PSDB; ABL53375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial lichenase
                                    Rodriguez Munoz V,
                                                                         WPI; 2002-217195/27
                                                                                                                                                                                                                                                                                                                                    208 AA;
                                                                                            N-PSDB; ABL53374.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The corresp, gene and the plant promoter region are inserted into an expression vector and used to transform barley cells. The transformants are used to regenerate barley plants which are useful in brewing. This protein accumulates in the ripe (but ungerminated) seeds. The proportion of these to malted seeds is increased therefore, without an unacceptable increase in viscosity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soil bacterium; enzyme; lichenase; endo-1,3/1,4-beta-glucanase; brewing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                                                                                                                                                                                                                                                                                                                                  Prepn. of barley plants expressing heat stable beta-glucanase - by transforming cells with appropriate vector then regeneration giving seeds useful in brewing without conversion to malt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 VSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.7%; Score 226; DB 11; 35.1%; Pred. No. 1.1e-13; tive 23; Mismatches 70;
                                                                                                                                                                                                                                                           Baumlein H;
Endo-beta-1,3-1,4-glucanase; barley; brewing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB76858 standard; Protein; 208 AA
                                                                                                                                                                                                                                                           Mendel R-R,
                                                                                                                                                                                                                       (DEAK ) AKAD WISSENSCHAFT DDR
                                                                                                                                                  88DD-0320082.
                                                                                                                                                                                  88DD-0320082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUL-2000; 2000ES-0001922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 35.1%
nes 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; ; p; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacterial lichenase #1
                                                                                                                                                                                                                                                           Borriss R, Wobus U,
                                                                                                                                                                                                                                                                                            WPI; 1990-210631/28.
N-PSDB; AAQ05167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 AA;
                                    Bacillus macerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200212511-A1
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                                                                                                                                                23-SEP-1988;
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                                                                                                           31-JAN-1990
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                                                                       DD275704-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches

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This sequence is the lichenase (licA) of Orpinomyces sp. strain PC-2 of the invention. The protein was purified from a fungus or a fungal culture or from a recombinant DNA molecule having a fungal lichenase coding sequence. The lichenase enzyme hydrolyses the beta-1,4-glucan bonds adjacent to beta-1,3-linked glucan bonds, but does not cleave beta-1,4-linked glucans. They can be used for the treatment of animal grain-containing feeds to improve nutrient availability and for treatment
                                                                                                                                                                                                              67 GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                                                                                                                                                    139 TKVQFNYYTNGAG---NHEKFADLGFDAANAYHTYAFDWQPNSIKWYVDGQ-LKHTATTQ 194
                                                                                                                                                    Gaps
                                                                                                                                                                                     7 FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lichenase; lich; fungus; enzyme; beta-1,4-glucan bond hydrolysation; beta-1,3-linked glucan bond; grain-containing feed; grain treatment; nutrient availability; brewing; fermentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated lichenase protein - is obtained from Orpinomyces PC-2 used for treatment of grain to improve feeds or to improve brewing
                                                                                                                                                  11;
                                                                                                              Length 237;
     prods., e
See also
                                                                                                   Score 220.5; DB 11; Leuy...
Pred. No. 3.9e-13;
Transtahes 75; Indels
                                                                                                                                                                                                                                                                                                                                    127 VSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                                                                                                                                                                                                                                                                                                                                             : | | : | | : | | : | | : | | 195 IPAAPGK--IMMNLWNGTGVDDWLGSYNGVN-PIYAHYHWMRYRK 236
   thus this enzyme can be used in the mfr. of food beer and animal feed (e.g.for feeding poultry).
                                                                                                                                                  23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "mature lichenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "signal peptide"
30..246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 24-25; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW37884 standard; Protein; 245
                                                                                                                15.3%;
33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li X, Ljungdahl LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US17811
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                                                                                           Query Match
Best Local Similarity 33...
Best 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                            237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lichenase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAV29067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-1997;
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                                                                            Sequence
                                      AAQ05833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
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/label=amino-terminal half of B.macerans beta-glucanase
                                                                                                                                                                                                          GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVFWTVDGQEVRKT 122
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131..234
/label=carboxyl-terminal half of B.amyloliquefaciens
                                                                                                                                                                                   3 SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIALGRPWVEVDIEVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vonwettstein D;
enzyme with lichenase/endo-1,3/1,4-beta-glucanase (E.C. 3.2.1.73) activity. The enzyme is useful in brewing and for degrading beta-glucanases that cause problems during filtration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New thermostable (1,3-1,4)-beta-glucanase - prepd. using hybrid gene obtd. using Bacillus amyloliquefaciens and B.macerans genes
                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hybrid pre-beta-glucanase; glucans; beer; animal feed; poultry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This hybrid protein is encoded by the beta-glucanase-H2 gene. Following processing of the signal peptide the mature protein is produced, comprising the amino terminus of the B.macerans beta-glucanase and the carboxyl-terminal half of the B.amylo-liquefaciens beta-glucanase. This hybrid protein is thermostable and hydrolyses beta-glycosidic linkages in (1,3-1,4)-beta-glucans. Reducing sugars are obtd. at high temps. and
                                                                                                            Length 214;
                                                                                                                                                 Indels
                                                                                                                                                 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borriss R, Hofemeister J, Thomsen KK, Olsen O,
                                                                                                          15.6%; Score 225; DB 23; 36.2%; Pred. No. 1.2e-13; ive 21; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus amyloliquefaciens, Bacillus macerans.
                                                                                                                                                                                                                                                                                                                                EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFD 153
                                                                                                                                                                                                                                                                                                                                                                  176 ATTQIPAAPGK -- IMMNLWNGTGVDDWLGSYN 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hybrid (1,3-1,4)-pre-beta-glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; page 28; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR06622 standard; protein; 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CARL-) CARLSBERG A/S.
(DEAK ) AKAD WISSENSCHAFT DDR
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                                                                                                                            Best Local Similarity 36.28
Matches 55; Conservative
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                                                                        214 AA;
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                                                                                                            Query Match
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26-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                            59 IEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQE 118
of grain (e.g. barley or wheat) in the brewing and fermentation industries to increase carbon substrate availability and to maximise production of desired products.
                                                                              76; Indels 22; Gaps
                                                                                                  KDFSGAELYTLEEVQ-----YGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVD 58
                                                          Query Match 13.1%; Score 189; DB 19; Length 245; Best Local Similarity 32.9%; Pred. No. 4.7e-10; Matches 56; Conservative 16; Mismatches 76; Indels 2
                                                                                                                                                                               119 VRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWV 166
                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 61207.
                                                                                                                                                                                                                                                    AAG48467 standard; Protein; 282 AA
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990S-0123180.
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                                       245 AA;
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09-MAR-1999

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01-APR-1999

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16-APR-1999

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11-MAY-1999
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The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value sequences by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                 QEVRKTEGGQVSNL--TGTQGLRF--NLWSSESAAWVG---QFDESKLPLFQFINWVKVY 169
                                                                                                                                                                                 EVLGK -- - NPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDG 116
                                                                                                                                                                                                                                                                                                            165 IPIREFKNSEALGVPFPKHQPMRLYASLWEAEHWATRGGLEKTDWSKAPFTAFYRNYNVD 224
                                                                                                                                                               2 VSAKDFSGAELYTLEEVQYGKFEARMKMAA--ASGTVSSMFLYQNGSEIADGRPWVEVDI 59
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                                                                                                                                  Indels
                                                                                                     12.8%; Score 184; DB 21; 27.6%; Pred. No. 1.8e-09;
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                                                                                                                                 Mismatches
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                                                                                                                                          :| |||: ::| ||||| :|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||
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                                       / Match 12.8%; Score 184; DB 23; Local Similarity 27.6%; Pred. No. 1.8e-09; les 59; Conservative 33; Mismatches 98;
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                                                                                                                       Indels
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                                                                                           12.0%; Score 172; DB 21; 25.9%; Pred. No. 2.6e-08;
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           990S-0161361.
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990S-0161992.
990S-0161993.
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                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weidler M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
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                                                                                                           Similarity
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           26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
29-0CT-1999;
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                                                                                                                       63;
                                                                                                                                                                                                                                                                                                                                                                      FNG
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                                                                                            Query Match
                                                                                                           Local
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                   11 - MAY - 1999;
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29-JUN-1999;
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06-JUL-1999;
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                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                      :| : :| | | ; | | ; | | ; | | ; | | 114 SGHPYTLHTNVYT-KGTGDKEQQFHLWFDPTVN--FHTYCITWNPQRIIFTVDGIPIREF 170
                                                                                                                                                                                                            60 SGSGFQSNQEFLYGKAEVQMKLVPGNSAGTVTTFYLK-----SPGTTWDEIDFEFLGNI 113
                                                                                                                             --NPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                               EGGQVSNL--TGTQGLRF--NLWSSESAAWVG---QFDESKLPLFQFINWVKVYKYTPGQ 175
                                                                                                                                                                                                 176 GEGGSDFTLDWTDNFDTFDGSRWGKGDWTFDGNRVDLTDKNIYSRDGMLILALTRKGQES 235
                                                                         Gaps
                                                                                          SGAELYTLEEVQYGKFEARMKMAA - - ASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGK - 64
                                                                                                                                                                                171 KNPEAIGVPFPTRQPMRLYASLWEAEHWATRGGLEKTDWSKAPFTAF----YR----
                                                                         58;
                                                       12.0%; Score 172; DB 23; Length 282; 25.9%; Pred. No. 2.6e-08; Indels 5:ive 34; Mismatches 88; Indels 5
                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 66212.
                                                                                                                                                                                                                                                                                                 AAG52114 standard; Protein; 277 AA.
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990S-0126785
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                                                  Query Match
Best Local Similarity 25.99
Watches 63; Conservative
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                                      282 AA;
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05-MAR-1999,
23-MAR-1999,
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16-APR-1999,
116-APR-1999,
123-APR-1999,
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04-MAY-1999;
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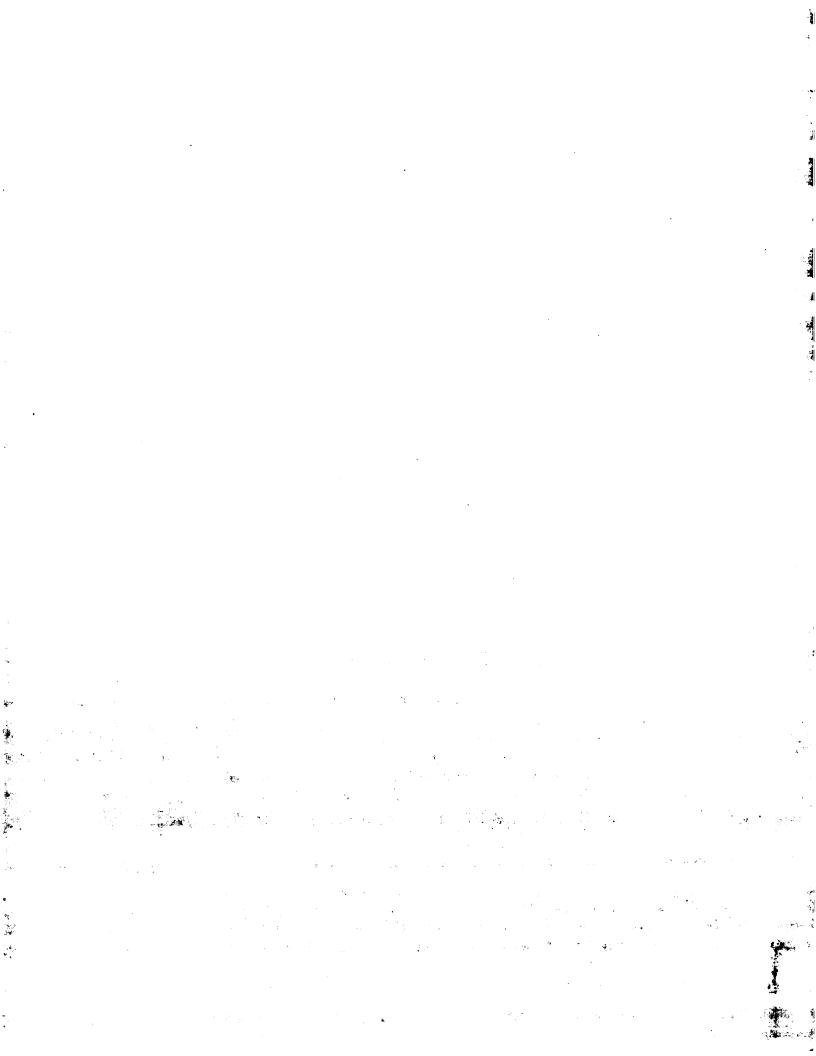
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30-AUG-1999
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Search completed: January Job time: 28.8125 secs

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                                                                                                                                                                                                                                                                                          EGGQVSNLTGTQGLRF-----NLWSSESAAWVG---QFDESKLPLFQFIN---- 164
                                                                                                                                                                                                      SGAELYTLEEVQYGKFEARMKMAA--ASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGK- 64
                                                                                                                                                                                  41;
                                                                                                                                                              DB 21; Length 277;
                                                                                                                                                                                  70; Indels
                                                                                                                                                            11.9%; Score 171.5; DB 2 27.0%; Pred. No. 2.8e-08; ive 32; Mismatches 70
           99US-0160980.
99US-0160981.
99US-0160989.
99US-0161405.
99US-0161359.
99US-0161360.
99US-0161361.
99US-0161361.
99US-0161363.
                                                                                                                                                                       Best Local Similarity 27.0
Matches 53; Conservative
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                                                                                                                                                                                                                                                                                                                                                        GCVWVNGKSVCPANSQ 235
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
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Q9fi31 arabidopsis
O80803 arabidopsis
Q9m0d1 arabidopsis
Q9m0d2 arabidopsis
                                                                                                                                           042800 aspergillus
060039 thermotoga
018910 arabidopsis
04K18 arabidopsis
08w4m6 arabidopsis
09su4 arabidopsis
09su4 arabidopsis
09bqu1 aspergillus
02by101 aspergillus
02by101 arabidopsis
038907 arabidopsis
                                                                                                          Q9wxnl thermotoga
Q94a49 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                            Q8xnf8 clostridium
Q39148 arabidopsis
Q93ui2 uncultured
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Q9fkl9 arabidopsis
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P93669 hordeum vul
Q949i0 festuca pra
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Q9kwf3 clostridium
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Nucleic Acids Res. 28:4317-4331(2000).

HSSP: P23904; 1AJK.

InterPro: IPR0001899; Glyco_hydro_16.

InterPro: IPR001899; Gram_pos_anchor.

Pfam; PF0072; Glyco_hydro_16; 3.

Pfam; PF0072; Glyco_hydro_16; 3.

PFNNTS; PR00737; GLHYDRASS16.

PROSITE; PS01034; GLYCOSIL_HYDROL_F16; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DCT-2001 (TrEMBLrel. 19, Last annotation update)
Endo-beta-1,3-1,4 glucanase (licheninase) (EC 3.2.1.73).
BGLS OR BH3232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ase; Complete proteome.
98142 MW; C1C4F0F158400285 CRC64;
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09WXN1
094A49
042800
060039
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08WAM6
09CSU4
09HC01
09P420
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P93669
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STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; Pubmed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase, Glycosidase, Complete
SEQUENCE 851 AA, 98142 MW, Cl
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Matches 82; Conservative
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                                                                                                      Bacillus halodurans.
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Q9K7X5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q93uil uncultured
Q8u8n5 agrobacteri
Q98c78 rhizobium 1
Q9k7x6 bacillus ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9k7x5 bacillus ha
Q9apd8 bacillus ci
Q45648 bacillus sp
                                                                                                                                                                 (without alignments)
2312.009 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                           January 9, 2003, 12:13:37; Search time 22.1019 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                            67.1580
                 GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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                                                                                                   protein search, using sw model
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Q9APD8
Q45648
Q93GE8
Q9S310
Q93GE7
Q93GE6
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Q9FDC9
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sp_unclassified?*
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sp_human:*
sp_invertebrate:*
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Maximum Match 100%
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sp_organelle:*
sp_phage:*
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sp_bacteriap:*
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sp_bacteria:*
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length: 2000000000
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sp_rodent:*
sp_virus:*
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MEDLINE-94288605; PubMed-7517127;
Tabernero C., Coll P.M., Fernandez-Abalos J.M., Perez P.,
Tabernero C., Coll P.M., Fernandez-Abalos J.M., Perez P.,
Santamaria R.I.,
"Cloning and DNA sequencing of bgaA, a gene encoding an endo-beta-1,3-
1, 4-glucanase, from an alkalophilic Bacillus strain (N137).";
Appl. Environ. Microbiol. 60:1213-1220(1994).
HSSP: P23944; IAJK.
HSSP: P23944; IAJK.
InterPro; IRROMO757; Glyco_hydro_16.
PRINTS: PRO0737; GLHYDRLASE16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 TKIQFNYFTNGVGG---NEHYHELGFDAADDFNTYAFEWRPESIRWFVNGELVHTA--- 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 SYNKFDCGENRSVQTYGYGPYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDIEFL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :: == <del>-</del>: = = -
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 VSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

ROdriguez V., Mellado R.P.;

Rodriguez V., Mellado R.P.;

"Novel lichenases from soil.";

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF254957; AAK50610.2;

EnterPro: IPR000757; Glyco_hydro_16.

Pfam; PF00722; Glyco_hydro_16; 1.

PROSITE; PS01034; GLYCOSYL_HYDROL_F16; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                             LICHENASE.
D047F8A34CA9EBE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER 1 1 SEQUENCE 214 AA; 24159 MW; 3DB186D3B9D991CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.2%; Score 242.5; DB 2;
35.5%; Pred. No. 2.7e-12;
Live 24; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                             18.6%; Score 247.5; DB 2; 36.1%; Pred. No. 1.5e-12; tive 20; Mismatches 75;
                                                                                                                                                                                                                                                                                                         PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
                                                                                                                                                                                                                                                                                                                                            POTENTIAL
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276 LI
: 31770 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                    Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uncultured bacterium.
                                                                                                                                                                                                                                                                                                                                                           32 2
276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 61; Conserv
                                                                        SEQUENCE FROM N.A.
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                                   NCBI_TaxID=1409;
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Matches
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                                                                                                                                                                                                                  ---TENIPQTPQKIMMNLWPGVGVDEWTGVFDGDNTPLHADYEWV---RYTPLEALDEEE 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQA--FHTYGLEWTPNYVRWTVDGQEVR 120
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                                                 KNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTE
                                                                                                                          GGQVSNLTGT - QGLRFNLWSSESA - AWVGQFDESKLPLFQFINWVKVYKYTP - - - - GQGE
                                                                                                                                                                                              178 GGSDFTLDWT--------DNFDTFDGSRWG-KGDWTFDGNRVDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KTEGGQVSNLTGTQG-LRFNLWSSESAA--WVGQFDESKLPLFQFINWVKVYKYTP 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Bacillaceae; Bacillus.
NCBI_TaxID=1397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.6%; Score 248.5; DB 2; Length 256; 34.7%; Pred. No. 1.1e-12; ive 28; Mismatches 70; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee D.-S., Kim J.-Y., Kim H.-B.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; A4306531; A4653947.1; -.
HSSP; P23904; IAJK.
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PR00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRASE16.
PROSTTE; PS01034; GLHYCOSYL, HYDROL_F16; 1.
SEQUENCE 256 AA; 27604 WW; 989ES0C09F6E4531 CRC64;
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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Last annotation update)
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BGLBC1.
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aurilia V., Martin J.C., Munro C.A., Mercer D.K., Flint H.J.; "Organisation and strain distribution of genes responsible for the utilization of xylans by the rumen cellulolytic bacterium Ruminococcus flavefaciens 17.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 GKDTTKVQFNYYTNGAG---NHEKLADLGFDAANAYHTYAFDWQPNSIKWYVDGQ-LKHT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAMILY 11 XYLANASE /FAMILY 16 BETA (1,3-1,4) GLUCANASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group; Clcstridia; Clostridiales; Lachnospiraceae; Ruminococcus. NCBL_TaxID=1265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases. |
| Submitter | Submitted | 
                                        123 EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 VSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               744 TODIPKTPGKIMMNAWPGLTVDDWLKAFN-GRTPLTAHYQWVTYNK 738
                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DTN-2002 (TrEMBLrel. 21, Last annotation update)
Family 11 xylanase /family 16 beta (1,3-1,4) glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F36BC68805FC5274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Endo 1-3,1-4-beta-glucanase (Fragment).
uncultured bacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.2%; Score 242.5; DB 2
34.9%; Pred. No. 1.6e-11;
Live 21; Mismatches 74
                                                                                                                                                                                     802 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 AA
                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; environmental samples.
NCBI_TaxID=77133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  802 AA; 89019 MW;
                                                                                                                                                                                                                                                                                                                               Ruminococcus flavefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 34.9
nes 58; Conservative
                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                         RESULT 5
Q9S310
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Q93GE7
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 SYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDIESL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       11;
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                                                                                                                                                                                                                                                                                                                                              18.1%; Score 241.5; DB 2; Length 214; 35.5%; Pred. No. 3.3e-12; ive 24; Mismatches 74; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.7%; Score 235.5; DB 2; Length 214; 35.5%; Pred. No. 1e-11; Live 23; Mismatches 75; Indels 11
1 [1]
SEQUENCE FROM N.A.
RAdiguez V., Mellado R.P.;
R Novel lichenases from soil.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
E MBL; AF254959; AAK50612.2;
R InterPro; IPR000757; Glyco_hydro_16;
R Ffam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
DR PROSITE; PS01034; GLYCOSYL_HYDROL_F16; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 ATTQIPAAPGK--IMMNLWNGTGVDDWLGSYNGVN-PLYAHYDWVRYTK 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 ATTOVPAAPGK -- IMMNLWNGTGVDDWLGSYNGVN-PLYAHYDWVRYTK 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rodriguez V., Mellado R.P.;
"Novel lichenases from soil.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR564961; AR450614.2;
InterPro: IRR000757; Glyco_hydro_16.
Pfan; PF00722; Glyco_hydro_16; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; UNKNOWN_1.
                                                                                                                                                                                                                                                                                               SEQUENCE 214 AA; 24175 MW; 3DB192D2F6B4CAA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 AA; 24131 MW; 1E9D8BFA4300EBA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endo 1-3,1-4-beta-glucanase (Fragment).
uncultured bacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; environmental samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 35.59
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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InterPro; IPR000757; Glyco_hydro_16
                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta-(1,3-1,4)-glucanase precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcaceae; Streptococcus.
NCBI_TaxID=1315;
                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-1406;
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SEQUENCE
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                                                                                                                                                            RESULT 10
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9
                                                                                                                                                                                                                                                                                  Van Rensburg P., van Zyl W.H., Pretorius I.S.;
van Rensburg P., van Zyl W.H., Pretorius I.S.;
"Over-expression of the Saccharomyces cerevisiae exo-beta-1,3-
glucanase gene together with the Butyrivibrio fibrisolvens endo-beta-
1,4-glucanase gene and the Bacillus subtlis endo-beta-1,3-1,4-
glucanase gene in Saccharomyces cerevisiae.";
submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; u60830; AABG5759.1; --
HSSP; PZ7051; 1G8C.
InterPro: IPR000757; Glyco_hydro_16.
PFam; PF00725; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRALSE16.
PROSITE: PS01034; GLYCOSYL_HYDROL_F16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 SYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDIEFL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 GKNPGSFQSNIITGKAGAQKTSEKHHAVSPA---ADQAFHTYGLEWTPNYVRWTVDGQEV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKDTTKVQFNYYTNGA-----ENHEKLADLGFDAANAYHTYAFDWQPNSIKWYVDWQ-L 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.6%; Score 234.5; DB 2; Length 239; 33.7%; Pred. No. 1.4e-11; ive 26; Mismatches 71; Indels 17;
                                                                                                                           Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | |: | |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 RKTEGGQVSNLTGTQGLRFNLWSSESAA-WVGQFDESKLPLFQFINWVKVYK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.4%; Score 232.5; DB 2; Length 242; 34.9%; Pred. No. 2.1e-11; ive 24; Mismatches 75; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Bacillaceae; Bacillus. NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sun J., Li W., Gu S., Xu Z., Zhao H., Xiao J.;
Submitred (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF499978; AAM03388.1;
SEQUENCE 242 AA, 27238 MW; 285FED3FE76AE69A CRC64;
                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Endo-beta-1,3-1,4-glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, Beta 1, 3-1, 4-glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 33.7%
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       STRAIN-NCIB 8565;
                                                                                                                                                                                                 NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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Q8RMP0
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140 GKDTTKVQENYYTNGAG---NHEKIVDLGFDAANAYHTYAFDWQPNSIKWYVDGQ-LKHT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 TKVQFNYYTNGIGGH---EKVVDLGFDASSGFHTYAFDWQPGYIKWYVDG-VLKHT---A 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ekinci. M., Flint H.J.;
"Isolation and overexpression of a gene encoding an extracellular beta-(1,3-1,4)-glucanase from Streptococcus bovis JB1.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 292911; CABD7443.1; -.
HSSP; P23904; 1AJK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endo-1,3-1,4-beta-glucanase (Fragment).
Paenthbacillus polymyxa (Bacillus polymyxa).
Bacteria; FirmLcutes; Bacillus/Clostridium group; Bacillales;
Paenibacillaceae; Paenibacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 212;
                                                                                                                                                               123 EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 17.3%; Score 230; DB 2; Length 21 Best Local Similarity 35.1%; Pred. No. 2.9e-11; Matches 59; Conservative 23; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yao W., Wang Y., Song W., Yang K., Su Z.;
"Gene cloning of an antifugal protein.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF284449; AAG02415.1; -.
HSSP; P23904; 1AJK.
                                                                                                                                                                                                                                                   196 ATNQIPTTPGK--IMMNLWNGTGVDERLGSYNGVN-PLYAHYDWVRYTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24127 MW; 7E707E7FBEF7A440 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 AA
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PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
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RESULT 13
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8
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MEDLINE=2135925; PubMed=11466286;
Moelling J., Breton G., Obloga J., Qlu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
EMBL; AE007778; ARR80751.1; -.
                                                                                                                                                                                                            138 TKVQFNYYT---SGQGNHEYLYNLGFDASQGFHTYGFDMQADHITWYVDSRAVYTA---- 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVIJGQEVRKTEGGQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 GSFQSNIITGKAGAQKTSEKH---HAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 YAGGEYRSNNRYGYGLYRVSMKPAKHIGVDSSFFSYTGPS----DNNPWDEIDIEFLGKDT 147
                                                                                                                              Gaps
                                                                                                                                                  7 FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPW/EVDIEVLGKNP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---TSNIPTHPGKVMMNLWPGIGVDSWLGAYD-GVTPVKAYYNWA---MYNP 245
                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGOVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYXYTP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 246;
                                                                                                     Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.6%; Score 221; DB 16; Length 2 33.7%; Pred. No. 1.9e-10; Indels ive 19; Mismatches 73; Indels
                                                                                                                            69; Indels
                                                        POTENTIAL.
BETA-(1,3-1,4)-GLUCANASE.
7DEF5BCE53790470 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 AA; 27717 MW; COEBC302678D2FE1 CRC64;
                                                                                                                                                                                                                                                           127 VSNLTGTQG-LRFNLW--SSESAAWVGQFDESKLPLFQFINWV 166
                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 18, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                    17.3%; Score 230; DB 2;
33.1%; Pred. No. 3.3e-11;
tive 26; Mismatches 69;
                                                                                                                                                                                                                                                                                                                            246 AA
InterPro; IPR000757; Glyco_hydro_16.
PRIMT: PR00722; Glyco_hydro_16; 1.
PRIMTS: PR00737; GLHYDRLABE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000757; Glyco_hydro_16.
PRIMTS; PR00721; Glyco_hydro_16; 1.
PRIMTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Last and Endo-1,3(4)-beta-glucanase family 16. CAC2807.
                                                                                                                                                                                                                                                                                                                            PRT;
                                                    24
237
26989 MW;
                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium acetobutylicum
                                                                                                               Best Local Similarity 33.1
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58; Conservative
                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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25
237 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1488;
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01-0CT-2001
                                                                                SEQUENCE
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                                                        SIGNAL
                                               Signal.
                                                                     CHAIN
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GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The genome of the natural genetic engineer Agrobacterium tumefaciens {\sf C58.^n};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=2160856); PubMed=11743193; Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphinmachak C., Wu Z., Romero P., Gordon D., Slang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Klm S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Endo-1,3-1,4-beta-glycanaes
Exox OR ATU4055 OR AGR_L_1600.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.4%; Score 219; DB 2; Length 205; 36.2%; Pred. No. 2.2e-10; ive 20; Mismatches 67; Indels 10;
                                                                                                                                                                                                                                                                                   Rodriquez V., Mellado R.P.;
"Novel lichenases from soil.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF254960; AAK50613.1;
InterPro; IRR007757; Glyco,hydro_16.
Pfam; PF00722; Glyco,hydro_16; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22890 MW; E7CADAAFE02A2F51 CRC64;
                                                                                 Last sequence update)
Last annotation update)
        AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 ATTOVPAAPGK -- IMMNLWNGTGVDDWLGSYN 197
     205
                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Last annota
Endo 1-3,1-4-beta-glucanase (Fragment).
                                                      Created)
     PRT;
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                                                                                                                                                                                    Bacteria; environmental samples.
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                                                                                 (TrEMBLrel. 19, (TrEMBLrel. 20,
                                                   (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55; Conservative
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     PRELIMINARY;
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NCBI_TaxID=176299;
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                                                                                                                                                              uncultured bacterium.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                               NCBI_TaxID=77133;
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01-DEC-2001
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NON_TER
SEQUENCE
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Q93UI1
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Q8U8N5
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EMBL, AP003006; BAB51743.1;

EMBL, AP003006; BAB51743.1;

Enterpro; IPR000755; Glyco_hydro_16;

Pfam: PF00722; Glyco_hydro_16;

PRINTS; PR00737; GLHYDRLASE16.
                   MEDLINE-2160851; PubMed=11743194; Godoner B., Hinkle G., Gattung S., Miller N., Blanchard M., Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Goodner B., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Lartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.; Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tunefaciens C58."; Science 294:2333-2336(2001).
EMBL: AE009336; AAL44856.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NPGSFQSN-IITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTE 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 KDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGK
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
SEQUENCE 289 AA; 32368 MW; 0384C6F83320EAC9 CRC64;
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SEQUENCE 293 AA; 32347 MW; 93BBA1672176ED3C CRC64;
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Last sequence update)
Last annotation update)
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35.1%; Pred. No. 4.1e-09;
tive 26; Mismatches 56;
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llarity 33.8%; Pred. No. 1.3e-08;
Conservative 27; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 GGQVSNLT----GTQGLRFNLWSSESAA-WVGQF 152
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MEDLINE-21082930; PubMed-11214968;
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01-0CT-2001 (TrEMBLrel. 18, L
01-0CT-2001 (TrEMBLrel. 18, L
Endo-1,3-1,4-beta-glycanase,
MLRS264.
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ses 51; Conserv
SEQUENCE FROM N.A.
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Qy 123 EGGQVSNLTGTQGLRFNLWSSES-AAWVGQF 152

Db 225 DPAKLP--SHAQKIFFSLWGSETMKGWMGAF 253

Search completed: January 9, 2003, 12:18:10 Job time : 24.1019 secs

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Sequence 83340, Application US/09724676 GENERAL INFORMATION:
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Sequence 83340, A
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                                                                        time 10.9074 Seconds alignments)
Million cell updates,
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Compugen Ltd
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5-09-724-676-83343
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US-09-724-676-83343
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US-09-724-676A-83342
US-09-724-676A-60984
US-09-917-384A-5
US-09-917-384A-5
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US-09-917-384A-1
US-09-917-384A-1
US-09-917-384A-1
US-01-293-418-1920
US-10-293-418-1920
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 version 5
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Maximum Match 100%
Listing first 45 summaries
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Sequence 3, Application US/10294561
Sequence 3, Application US/10294561
GENERAL INFORMATION:
APPLICANT: Seikagaku Corporation
TITLE OF INVENTION: (1-3)-Beta-D-Glucan Binding Domain Protein, Measuring Method (
TITLE OF INVENTION: (2)-1918
FILE REFERENCE: 072918
FILE REFERENCE: 072918
CURRENT PAPLICATION NUMBER: US/10/294,561
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: JP 2001-351943
PRIOR APPLICATION NUMBER: JP 2001-351943
SOGTWARE: Patentin version 3.1
SQD ID NOS: 5
SOFTWARE: Patentin version 3.1
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Pred. No. 0.014;
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US-10-294-561-3
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Best Local Similarity
Matches 61; Conserv
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US-09-724-676-83340
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; ORGANISM: Homo sapiens
US-09-724-676-83341
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US-09-724-676A-83341
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Best Local Similarity
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US-09-724-676A-83341
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               TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION NUMBER: US/09/724,676 CURRENT FILING DATE: 2000-11-28 NUMBER OF EQ. ID NOS: 97222 SOFTWARE: Patentin version 3.2 SEQ ID NO 83340
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REPERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 83340
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CORGANISM: Homo sapiens
US-09-724-676-83340
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; ORGANISM: Homo sapiens
US-09-724-676A-83340
APPLICANT: Compugen LTD
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 83341
LENGTH: 1554
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20.8%; Pred. No. 0.7;
:ive 36; Mismatches
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20.8%; Pred. No. 0.7;
tive 36; Mismatches
                                                          -- VDLTDKNIYSRDGMLILA
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                                                                                                                                                                                                                                                                    ; Sequence 83341, Application US/09724676; GENERAL INFORMATION:
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Best Local Similarity 20.8%
Matches 46; Conservative
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131 TGTQGLRFNLWSSESAAWVGQFDESKLPLFQFINWV	Query Match Best Local Similar Matches 59; Con
DD 1315 HGLLKTEABSYEGLLAFSLIPKNWPDQGRIQIQNLSVRYDSSLRFVLKHVNAL 1367 Qy 167 KVYKYTPGQGEGGSDFTLDWTDNFDTFDGSRWG 199	Qy 12 LYTLEEVQY
:    :     :	Db 1210 LTTIRAFRYE
RESULT 6	
US-09-124-6/6-88343 ; Sequence 83343, Application US/09724676 ; CEMPEAT INFORMATION.	Qy 131 TGT
; GENERAL INFORMATION: ; APPLICANT: Compugen LTD ; TITLE OF INVENTION: United of alternative enlicing	Db 1315 HGLLKTEAES
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CURRENT FILING DATE: 2000-11-28 : NUMBER OF SEO ID NOS: 97222	Db 1375 RPPAPSLIPK
; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 83343	Qy 178 GGSDFTLDWT
LENGTH: 1558	Db 1431 GKSSFSLAFF
) ORGANISM: Homo sapiens US-09-724-676-83343	Qy 213 TDKNIYSRDG
Query Match 7.4%; Score 99; DB 5; Length 1558;	Db 1491 ATENILOKVV
æ	RESULT 8
YONGS	US-09-724-676-83344 ; Sequence 83344, Ap
	GENERAL INFORMATIO HPPLICANT: COMPUG
OY 71 SNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVYRKTEGGQVSNL 130	; TITLE OF INVENTIO ; FILE REFERENCE: 1
DD 1256 ACVVLIAAVTSISNSLHRELSAGLVGLGLTYAL-MVSNYLNWMVRNLADMELQLGAVKRI 1314	; CURRENT APPLICATI ; CURRENT FILING DA
Oy 131 TGTOGLRFNLWSSESAAWVG	; NUMBER OF SEQ ID ; SOFTWARE: PatentI
DD 1315 HGLLKTEAESYEGLLGERLRERGGEESKEECVWVGGHKGAWGWGGTFCYSCGPCLVLSPA 1374	; SEQ ID NO 83344 ; LENGTH: 1602
Qy 151GE 177	; TYPE: PRT ; ORGANISM: HOMO S
DD 1375 RPPAPSLIPKNWPDQCKIQIQNLSVRYDSSLKPVLKHVNALISPGQKIGICGRTGS 1430	US-09-724-676-83344
178 GGSDFTLDWTDNFDTFDGSRWGKGDWTF-DGNRVDL	Query Match Best Local Similar Matches 51; Con
1431	Qy 12 LYTLEEVQY
IDANIISADGMETER   :     :	: :    Db 1210 LTIRAFRYE
BIGUM MATERIA TOTAL	Qy 71 SNIITGKAGA
RESULT 7 11S-104-724-676a-83343	:::   Db 1256 ACVVLIAAVT
; Sequence State of Sequence o	Qy 131 TGT
; APPLICANT COMPUGED LTD ; TITLE OF INVENTION. Variants of alternative enlicing	Db 1315 HGLLKTEAES
	Оу 151
; CURRENT FILING DATE: 2000-11-28 ; NUMBER OF SEO ID NOS: 97222	Db 1375 RPPAPSLIPK
; SOFTWARE: Patentin version 3.2	QY 178 GGSDFTLDWT
; JEN 0 03343 ; LENG 03343 ; TYPE: DPM	Db 1431 GKSSFSLAFF
	RESULT 9 US-09-724-676A-83344

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                                                                                                                                              AGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNL 130
                                                                                                                                                                                                                    ----QGL------RFNLWSSESAAWVG------150
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::| | |:::| |
                                       Gaps
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                                                                        QY-GKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQ 70
                                                                                                                                                                                                                                                                                           ------GEDESKLPLFQFINWVKVYKYTPGO------GE
7.4%; Score 99; DB 5; Length 1558;
18.7%; Pred. No. 1.8;
tive 38; Mismatches 100; Indels 118;
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larity 19.5%; Pred. No. 2.1;
Conservative 33; Mismatches 85; Indels 93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pugen LTD
TYION: Variants of alternative splicing
S: 129181.4 Compugen
ATION NUMBER: US/09/724,676
ATION SI 2000-11-28
ID NOS: 97222
antin version 3.2
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Application US/09724676
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                  larity 18.7%
Conservative
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                                                                                                                                                                                                                                                                                      Length 1602;
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                                                                                                                                                                                                                                                                                                                         85; Indels
                                 APPLICANT: Compugen LTD
TILE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 83344
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SOFTANARE: Datentin version 3.2
                                                                                                                                                                                                                                                                                      7.4%; Score 98.5; DB 5; 19.5%; Pred. No. 2.1;
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19.4%; Pred. No. 2.6;
Live 33; Mismatches
Sequence 83344, Application US/09724676A
GENERAL INFORMATION:
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                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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US-09-724-676-83342
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Matches 50; Conserve
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US-09-724-676-83342
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-----QFDESKLPLFQFINWVKVYKYTPGQ-----GE 177
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                                                                                                                                                                                                           Sequence 83342. Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 83342
LENGTH: 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
7.3%; Score 97.5; DB 5;
Best Local Similarity 19.4%; Pred. No. 2.6;
Matches 50; Conservative 33; Mismatches 82;
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                                                                                                       178 GGSDFTLDWTDNFDTFDG 195
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US-09-724-676A-83342
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TYPE: PRT
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ORGANISM: Homo sapiens
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                                                                                            ----RPWVEVDIEVLGKNPG-SFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWT 106
                                                                                                                                                                                                               107 PNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSESAAWVGQFDESKLPLFQFINWV 166
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                                         Gaps
                                                                        2 VSAKDFSGA---ELYTLEEVQYGKF-EARMKMAAASGTV-SSMFLYQNGSEIADG---- 51
                                                                                                                                                                292 YGPYDPDEEVIVHAEGSYEGKTFKSNSVNVASASEK------
                                                                                                                                                                                                                                                                                  167 KVYKYTPGQGEGGSD--------FTLDWTDNFDTFDGSRWGKGDWTF-
                                      71; Indels 109;
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       Length 444;
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GENERAL INFORMATION:
APPLICANT: COmpugen LTD
TITLE OR INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 60984
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TITLE OF INVENTION: Variants of alternative splicing
FILE REPERBNCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
LENGTH: 486
       DB 6;
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Local Similarity 22.1%; Pred. No. 9.9;
les 30; Conservative
     Score 86.5; Di
Pred. No. 4.7;
                                      35; Mismatches
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US-09-724-676A-60984
; Sequence 60984, application US/09724676A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      206 ----DGN-----RVDLTDKNI--YSRDG 222
                                                                                                                                                                                                                                                                                                                                                                                      410 FLDKDGDLAGSYTVDIDDGYVTEYDEDG 437
     6.5%;
Query Match
Best Local Similarity 19.88
Matches 53; Conservative
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; ORGANISM: Homo sapiens
US-09-724-676-60984
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US-09-724-676-60984
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APPLICANT: DING, SHI-YOU
APPLICANT: DING, SHI-YOU
APPLICANT: MCCARTER, SUZANNE
APPLICANT: MCCARTER, SUZANNE
APPLICANT: WINZANT, TODD B.
TITLE OF INVENTION: THERMAL TOLERANT EXOGLUCANASE FROM ACIDOTHERMUS
TITLE OF INVENTION: CELLULOLYTICUS
FILE REFERENCE: NREL 01-38
CURRENT APPLICANION NUMBER: US/09/917,384A
CURRENT FILING DATE: 2001-07-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 9
LENGTH: 638
TYPE: PRT
                                                                                                                                                                                                                                                                                            145 SAAWV------GQFDESKLPLFQFINWVKVYKYTPG------QGEGGSDFTLDWTD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 GAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 NLWSSESAA---WVGQFDESKLPLFQFINWVKVYKYTPGQGEGGS---DFTLDWTDNFDT 192
                                                                                                                                                                             -TGTQGLRFNLWSSE 144
                                                                                                                                                                                                                    149 LHWKKVYLKAILRMKQLEDHEAFETSSLIGHSARVYALYYKDGLLCTGSDDLSAKLWDVS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
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                                                                                     Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 638;
                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5;
                                                                                       DB 5;
                                                                                     Query Match 6.3%; Score 83.5; Di
Best Local Similarity 22.1%; Pred. No. 9.9;
Matches 30; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.3%; Score 83.5; Di
Best Local Similarity 22.2%; Pred. No. 14;
Matches 36; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375 GATNSWNGNYGTPPAGDSTFYGMAYDWEPVY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9, 2003, 12:14:11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Acidothermus cellulolyticus US-09-917-384A-9
                                                                                                                                                                           103 LEWIPNYVRWTVDGQEVRKTEGGQVSNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09917384A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        189 NFDTFDGSRWGKGDWT 204
                                                                                                                                                                                                                                                                                                                                                                                    Search completed: January
Job time: 12.9074 secs
; TYPE: PRT
; ORGANISM: HOMO SE
US-09-724-676A-60984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-917-384A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193
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January 9, 2003, 12:05:16 ; Search time 6.31481 Seconds (without alignments) 761.932 Million cell updates/sec
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1333
1 MVSAKDFSGAELYTLEEVQY.....TRKGQESFNGQYPRDDEPAP 248
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                            118974 seqs, 19401057 residues
                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                              Searched:
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113974

Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 152, App	Sequence 6, Appli	Sequence 8, Appli		-	Sequence 6377, Ap	Sequence 4, Appli	Sequence 192, App	Sequence 178, App	Sequence 98, Appl	Sequence 1, Appli	Sequence 28, Appl	Sequence 6052, Ap	Sequence 2, Appli	Sequence 6, Appli	Sequence 150, App		Sequence 865, App	
	ID	US-09-734-569-152	US-09-988-200-6	US-09-988-200-8	US-09-738-363-2	US-09-738-363-4	US-09-738-626-6377	US-10-042-417-4	US-09-841-132-192	US-09-841-132-178	US-10-007-693-98	US-09-863-547B-1	US-09-734-569-28	US-09-738-626-6052	US-09-728-911-2	US-09-949-192-6	US-09-734-569-150	US-09-738-626-4312	US-09-925-299-865	US-09-738-626-4854
	DB	10	10	10	10							10					10	σ	10	თ
	Query Match Length DB	287	620	545	1385	1289	714	422	848	1530	1531	467	156	475	231	231	200	1233	165	731
ф	Query Match	9.6	89.	8.5	6.5	6.3	6.3	6.3	6.3	6.3	6.3	6.0	0.9	5.9	5.8	5.8	5.8	5.8	5.7	5.7
	Score	120	117	113	86.5	84.5	84	83.5	83.5	83.5	83.5	80.5	80	78.5	77.5	77.5	77	77	75.5	75.5
	Result No.		7	m	4	S	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19

Sequence 4, Appli Sequence 4876, Ap Sequence 61, Appl	Sequence 2, Appli Sequence 4, Appli	Sequence 3, Appli Sequence 11, Appl	Sequence 314, App Sequence 1, Appli	Sequence 13481, A Sequence 313, App	Sequence 3, Appli	Sequence 11, Appl	Sequence 5606, Ap	Sequence 50, Appl	Sequence 5852, Ap	Sequence 26, Appl	Sequence 5350, Ap	Seguence 12138, A	Sequence 2, Appli	Sequence 38, Appl	Seguence 1188, Ap	Sequence 5115, Ap	Sequence 25, Appl	Sequence 158, App	Sequence 13455, A
0 US-09-740-274-4 US-09-738-626-4876 0 US-09-778-927A-61	2 US-10-100-912-2 0 US-09-452-380-4	0 US-09-452-380-3 0 US-09-289-346A-11	U US-09-801-358-314 O US-09-833-435A-1	0 US-09-815-242-13481 0 US-09-764-870-313	US-10-094-080-3	US-09-964-899-11	US-09-738-626-5606	0 US-09-854-122-50	US-09-738-626-5852	0 US-09-215-450-26	0 US-09-815-242-5350	0 US-09-815-242-12138	0 US-09-332-226-2	0 US-09-866-562-38	0 US-09-925-300-1188	US-09-738-626-5115	0 US-09-905-176-25	0 US-09-765-272-158	0 US-09-815-242-13455
1375 1 245 9 2167 1	925 1	326 356 356	6/8 1 862 1	930 1 707	395 9	433 9	511 9	700 I	1054 9	406 1	663 1	663 1	915 1	1050	345 1	350 9	420 1	471 1	486 1
5.7 5.6 5.6	0.0. 0.0.	ນ ເບ ດີ ເບີ ເ	5.5 5.5	ა. გ. 4.	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.3	5.3	5.3	5.3	5.3
75.5 75 75	75	73.5	73.5	73.5	72	72	72	72	72	71.5	71.5	71.5	71.5	71.5	7.1	71	7.1	71	71
20 21 22	22.0	25 26 26	28	29 30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 US-09-134-569-152 Sequence 152, Application US/09734569 Patent No. US20020064816A1 GENERAL INFORMATION: APPLICANT: Lerchl, Jens APPLICANT: Ehrhardt, Thomas APPLICANT: Ehrhardt, Thomas APPLICANT: Ehrhardt, Thomas APPLICANT: Erend, Marcas APPLICANT: Erend, Andreas APPLICANT: Freund, Andreas APPLICANT: Freund, Annette APPLICANT: Schindld, Ralf-Michael APPLICANT: Marks APPLICANT: Marks APPLICANT: Marks APPLICANT: Marks APPLICANT: Schindld, Ralf-Michael APPLICANT: NEWRITON: in the synthesis of carbohydrates TITLE OF INVENTION: in the synthesis of carbohydrates CURRENT APPLICATION NUMBER: US 60/171,101 PRIOR FILING DATE: 1999-12-16 NUMBER OF SQL ID NOS: 181 SOFWARE: PATENTIN VOS: 121 SOFWARE: PATENTIN VOR: 2.1/WordPerfect 6.1	RESULT 1 US-09-734-569-152
Sequence 152, Application US/09734569 Patent No. US20020064816A1 GENERAL INFORMATION: APPLICANT: Lerchl, Jens APPLICANT: Erhardt, Thomas APPLICANT: Ehrhardt, Thomas APPLICANT: Reindi, Andreas APPLICANT: Reindi, Markers APPLICANT: Frank, Markers APPLICANT: Fround, Annette APPLICANT: Reski, Ralf-Michael APPLICANT: Reski, Ralf-Michael APPLICANT: Reski, Ralf-Michael APPLICANT: Reski, Ralf-Michael APPLICANT: Schmidt, Ralf-Michael APPLICANT: Reski, Ralf-Michael APPLICANT: BASF-NAE-1332-99-US CURRENT APPLICATION: In the synthesis of carbohydrates FILE REFERENCE: BASF-NAE-1332-99-US CURRENT APPLICATION NUMBER: US 60/171,101 PRIOR FILING DATE: 1999-12-16 NUMBER OF SEQ ID NOS: 181 SOFTWARE: Patentin Ver: 2.1/WordPerfect 6.1	
GENERAL INFORMATION: APPLICANT: Lerchl, Jens APPLICANT: Renz, Andreas APPLICANT: Enchard, Thomas APPLICANT: Enchard, Thomas APPLICANT: Cirpus, Petra APPLICANT: Cirpus, Petra APPLICANT: Frank, Markus APPLICANT: Frank, Markus APPLICANT: Frank, Markus APPLICANT: Frank, Markus APPLICANT: Schmidt, Ralf-Michael APPLICANT: Schmidt, Ralf-Michael APPLICANT: Seski, Ralf TITLE OF INVENTION: Moss genes from Physcomitralla patens encoding proteins TITLE OF INVENTION: Moss genes from Physcomitralla patens FILE REFERENCE: BASF-NAE-1332-99-US CURRENT APPLICATION NUMBER: US/09/734,569 CURRENT FILING DATE: 1999-12-16 NUMBER OF SEQ ID NOS: 181 SOFTWARKE: PATENT VET. 2.1./WordPerfect 6.1	Sequence 152, Application US/09734569
APPLICANT: Relat, Jens APPLICANT: Relat, Andreas APPLICANT: Relat, Thomas APPLICANT: Relat, Thomas APPLICANT: Relat, Thomas APPLICANT: Relat, Parreas APPLICANT: Cirpus, Petreas APPLICANT: Erank, Markus APPLICANT: Fraunk, Markus APPLICANT: Schnidt, Ralf Michael APPLICANT: Schnidt, Ralf Michael APPLICANT: Reski, Ralf TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins TITLE OF INVENTION: in the synthesis of carbohydrates TITLE OF INVENTION: in the synthesis of carbohydrates CURRENT APPLICATION NUMBER: US/09/734,569 CURRENT APPLICATION NUMBER: US/09/734,101 PRIOR FILING DATE: 1999-12-16 NUMBER OF SEQ ID NOS: 181 SOFTWARE: Patentin Ver: 2.1/WordPerfect 6.1	; GENERAL INFORMATION:
APPLICANT: Ehrhardt, Thomas APPLICANT: Reindl, Andreas APPLICANT: Cirpus, Padreas APPLICANT: Cirpus, Andreas APPLICANT: Eschoff, Friedrich APPLICANT: Bischoff, Friedrich APPLICANT: Frank, Markus APPLICANT: Schnidt, Ralf APPLICANT: Schnidt, Ralf Michael APPLICANT: Reski, Ralf TITLE OF INVENTION: In the synthesis of carbohydrates TITLE OF INVENTION: In the synthesis of carbohydrates CURRENT APPLICATION NUMBER: US/09/734,569 CURRENT APPLICATION NUMBER: US/09/734,569 PRIOR FILING DATE: 1999-12-16 NUMBER OF SEQ ID NOS: 181 SOFTWARE: Patentin Ver: 2.1/WordPerfect 6.1	; APPLICANT: LEFCOL, Jens ; APPLICANT: Renz, Andreas
APPLICANT: Reindl, Andreas APPLICANT: Cirpus, Petra APPLICANT: Cirpus, Petra APPLICANT: Frank, Markus APPLICANT: Frank, Annette APPLICANT: Frank, Annette APPLICANT: Schmidt, Ralf-Michael APPLICANT: Schmidt, Ralf-Michael APPLICANT: Beski, Ralf TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins TITLE OF INVENTION: Moss genes from Physcomitrella patens FILE REFERENCE: BASF-NAE-1332-99-US CURRENT PFLIANG NUMBER: US/09/734,569 CURRENT FILING DATE: 2001-05-24 PRIOR FILING DATE: 1999-12-16 NUMBER OF SEQ ID NOS: 181 SOFTWARE: Patentin Ver. 2.1.WordPerfect 6.1	
APPLICANT: CIPURA Anerkus APPLICANT: Bischoff Friedrich APPLICANT: Frank, Markus APPLICANT: Frank, Annette APPLICANT: Freund, Annette APPLICANT: Duwenig, Elke APPLICANT: Schmidt, Ralf-Michael APPLICANT: Schmidt, Ralf-Michael APPLICANT: Reski, Ralf TITLE OF INVENTION: Moss genes from Physcomitralla patens encoding proteins TITLE OF INVENTION: Moss genes from Physcomitralla patens encoding proteins FILE REFERENCE: BASF-NAE-1332-99-US CURRENT PELLOATION NUMBER: US/09/734,569 CURRENT FILING DATE: 1099-12-16 NUMBER OF SEQ ID NOS: 181 SOFTWARE: Patentin Ver: 2.1.WordPerfect 6.1	
APPLICANT: Frank, Markus APPLICANT: Freund, Annette APPLICANT: Freund, Annette APPLICANT: Duwenig, Elke APPLICANT: Committee APPLICANT: Schmidt, Ralf APPLICANT: Reski, Ralf TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins FILE REFERENCE: BASF-NAE-1332-99-US CURRENT PELLORION NUMBER: US/09/734,569 CURRENT FILING DATE: 2001-05-24 PRIOR FILING DATE: 1999-12-16 NUMBER OF SEQ ID NOS: 181 SOFTWARE: Patentin Ver: 2.1/WordPerfect 6.1	
APPLICANT: Freund, Annette APPLICANT: Duvenig, Elke APPLICANT: Duvenig, Elke APPLICANT: Colmidt, Ralf-Michael APPLICANT: Schmidt, Ralf-Michael APPLICANT: Reski, Ralf-Michael TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins FILE PERERROE: BASF-NAE-133-99-US CURRENT APPLICATION NUMBER: US/09/734,569 CURRENT FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 60/171,101 PRIOR FILING DATE: 1999-12-16 NUMBER OF SEQ ID NOS: 181 SOFTWARE: Patentin Ver: 2.1/WordPerfect 6.1	
APPLICANT: Duvenig, Elke APPLICANT: Schmidt, Ralf-Michael APPLICANT: Schmidt, Ralf-Michael APPLICANT: Schmidt, Ralf-Michael APPLICANT: Reski, Ralf TITLE OF INVENTION: in the synthesis of carbohydrates TITLE OF INVENTION: in the synthesis of carbohydrates CURRENT APPLICATION NUMBER: US/09/734,569 CURRENT APPLICATION NUMBER: US/09/734,101 PRIOR APPLICATION NUMBER: US 60/171,101 NUMBER: 1999-12-16 NUMBER OF SEQ ID NOS: 181 SOFTWARE: Patentin Ver: 2.1/WordPerfect 6.1	
APPLICANT: Schmidt, Ralf-Michael APPLICANT: Schmidt, Ralf-Michael APPLICANT: Reski, Ralf TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins TITLE OF INVENTION: in the synthesis of carbohydrates FILE REFERENCE: BASF-NAE-1332-99-US CURRENT APPLICATION NUMBER: US/09/734,569 CURRENT APPLICATION NUMBER: US 60/171,101 PRIOR FILING DATE: 1999-12-16 NUMBER OF SEQ ID NOS: 181 SOFTWARE: PatentIn Ver: 2.1/WordPerfect 6.1	
TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins; TITLE OF INVENTION: in the synthesis of carbohydrates; FILE OF INVENTION: in the synthesis of carbohydrates; FILE REFERENCE: BASF.NAE-1332-99.US; CURRENT APPLICATION NUMBER: US/09/734,569; CURRENT FILING DATE: 2001-05-24; PRIOR APPLICATION NUMBER: US 60/171,101; PRIOR FILING DATE: 1999-12-16; NUMBER OF SEQ ID NOS: 181.	
TITLE OF INVENTION: in the synthesis of carbohydrates FILE REFERENCE: BASF-NAE-132-99-US CURRENT APPLICATION NUMBER: US/09/734,569 CURRENT FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 60/171,101 PRIOR FILING DATE: 1999-12-16 NUMBER OF SEQ ID NOS: 181 SOFTWARE: PatentIn Ver: 2.1/WordPerfect 6.1	TITLE OF INTENTION: Moss genes from Physiconitrella patens encoding proteins
; FILE REFERENCE: BASF-NAE-1332-99-US ; CURRENT APPLICATION NUMBER: US/09/734,569 ; CURRENT FILING DATE: 2001-05-24 ; PRIOR APPLICATION NUMBER: US 60/171,101 ; PRIOR FILING DATE: 1999-12-16 ; NUMBER OF SEQ ID NOS: 181 ; SOFTWARE: PatentIn Ver: 2.1/WordPerfect 6.1	TITLE OF INVENTION: in the synthesis of carbohydrates
CURRENT APPLICATION NUMBER: US/09/734,569 CURRENT FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 60/171,101 PRIOR FILING DATE: 1999-12-16 NUMBER OF SEQ ID NOS: 181 SOFTWARE: Patentin Ver: 2.1/WordPerfect 6.1	; FILE REFERENCE: BASF-NAE-1332-99-US
; CURRENT FILING DATE: 2001-05-24 ; PRIOR APPLICATION NUMBER: US 60/171,101 ; PRIOR FILING DATE: 1999-12-16 ; NUMBER OF SEQ 10 NOS: 181 ; SOFTWARE: Patentin Ver: 2.1/WordPerfect 6.1	; CURRENT APPLICATION NUMBER: US/09/734,569
<pre>; PRIOR APPLICATION NUMBER: US 60/171,101 ; PRIOR FILING DATE: 1999-12-16 ; NUMBER OF SEQ ID NOS: 181 ; SOFTWARE: Patentin Ver: 2.1/WordPerfect 6.1</pre>	; CURRENT FILING DATE: 2001-05-24
<pre>; PKION FILING DATE: 1999-12-16 ; NUMBER OF SEQ ID NOS: 181 ; SOFTARNE: Patentin Ver: 2.1/WordPerfect 6.1</pre>	; PRIOR APPLICATION NUMBER: US 60/171,101
; NOMBER OF SEQ ID NOS: 181 ; SOFTWARE: PatentIn Ver. 2.1/WordPerfect 6.1	FRIOR FILING DATE: 1999-12-16
	, NOMBER OF SEQ ID NOS: 101 . SOFTWARE Datentin Ver 2 1/WordDerfect 6 1
; SEO ID NO 152	; SEO ID NO 152
; LENGTH: 287	; LENGTH: 287
; TYPE: PRT	TYPE: PRT
; OKGANISM: Physcomitrella patens US-09-734-569-152	; OKGANISM: Physcomitrella patens US-09-734-569-152
Query Match 9.0%; Score 120; DB 10; Length 287;	9.0%; Score 120; DB 10;
Best Local Similarity 23.0%; Pred. No. 0.00037; Matches 49; Conservative 30; Mismatches 70; Indels 64; Gaps 11	23.0%; Pred. No. 0.00037; tive 30; Mismatches 70; Indels 64;
YQNĞSELADGRPWV	
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QY 75 TGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGT- 133	75 TGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGT-
Db 123 VDGVGGRE-QQMYLGFDPSADFHYYRFRWSKDMVVFYVDNKPVRVFKNLEGTV 174	

involv

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AFFLICANT.
POTIN, Philippe
RICHARD, Christophe
RICHARD, Christophe
HENRISSAT, Bernard
YULN, Jean-Claude
KLOAREG, Bernard
TITLE OF INVENTION: Glycolyse hydrolase genes and their
use for producing enzymes for the blodegradation of
                                         112 WTVDGQEVRKTEG---GQVSNLTGTQGLR--FNLWSSE----SAAWVGQFDESKLPLFQF 162
                                                                     ---YHLPFDPRND--FHTYGVNVTKDKIT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GKNPGSFQSNI----ITGKAG------AQKTSEKHHAVSPAADQAFHTYG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSGAELYTLEEVQYGKFEARMKMA-AASGTVSSMFLYQN-GSEIADGRP-WVEVDIEVL- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DENNISON, MESEROLE, SCHEINER & SCHULTZ
STREET: 612 Crystal Square 4, 1745 Jefferson Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,200
FILING DATE: 19-No. US20020094553A1-2001
CLASSIFICATION: <a href="https://documents.org/line">documents.org/line</a>
APPLICATION NUMBER: 09/269,731
FILING DATE: <a href="https://documents.org/line">documents.org/line</a>
APPLICATION NUMBER: 69 12204
FILING DATE: 07-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.5%; Score 113; DB 10;
23.0%; Pred. No. 0.004;
iive 41; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: <Unknown>
REFERENCE/DOCKET NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (703) 412-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BARBEYRON, Tristan
349 HNIVVKNGKPTWMRPGSFPQTNHNG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09988200 Patent No. US20020094553A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 545 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (703) 412-1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: IRA SCHULTZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                 163 INWVKVYKYTPGQGEGGS 180
                                                                                                                                                                          RTWVKVGNNNSAPGEGOS 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: VIRGINIA COUNTRY: U.S.A. ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                             RESULT 3
US-09-988-200-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-988-200-8
                                                                                                                                                                          458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Glycolyse hydrolase genes and their use for producing enzymes for the biodegradation of carrageenans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                  -----QGLRFNLWSSESAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGSDFT 183
                                                       175 PGTKYLNQQAMGVXISIWDGSSWATQG----GRVP----INW------ASAPFT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 -EVLGKN-----PGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYR 111 :: | | | | | | | | | | :: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.8%; Score 117; DB 10; Length 620; 27.3%; Pred. No. 0.002; ive 23; Mismatches 73; Indels 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DENNISON, MESEROLE, SCHEINER & SCHULTZ
STREET: 612 Crystal Square 4, 1745 Jefferson Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 YGKFEARMKMAAASGTVSSMF-LYQ--NGSEIADGR-PWVEVDI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,200
FILING DATE: 19-No. US20020094553A1-2001
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: <Unknown>
REFERENCE/DOCKET NUMBER: <Unknown>
                                                                                                         LDWTDNFDTFDGSRWGKGDWTFDGNRVDLTDKN 216
                                                                                                                                                 215 ATYQ------DFALNGCVVDPNDPN 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: CUNKNOWN>
APPLICATION NUMBER: FR 96 12204
FILING DATE: 07-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/269,731
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                     RICHARD, Christophe
HENRISSAT, Bernard
YVIN, Jean-Claude
KLOAREG, Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 412-1155
TELEFAX: (703) 412-1161
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                           Sequence 6, Application US/09988200
Patent No. US20020094553A1
GENERAL INFORMATION:
APPLICANT: BARBEYRON, Tristan
POTIN, Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 620 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: IRA SCHULTZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22202
COMPUTER READABLE FORM:
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Best Local Similarity 27.34
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: VIRGINIA COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: ARLINGTON
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US-09-988-200-6
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Gaps

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1176 NGSIRSDISYQNIDAIVLPTLPKLRHWFMSDRFSEQGDIMAKFQGALNRAYAQLEQSTLL 1235
                                                                           1274 --VSQMIE----IENFNPDKEYNLVFHGQGEG--TVTLEHGEETKYIETHTHFANFTT 1324
                                             87 HHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSESA 146
                                                                                                                                     ---WTDNFDTFDG 195
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                                                                                                                                                                                                                                                   65;
                                                                                                                                                                                                                       SRWGKGDWTFDGNRVDLTDKNIYSRDGMLI --- LALTRKGQESFNGQVPRDDE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86;
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                                                                                                                                  147 AWVGQFDESKLPLFQFINWVKVYKYT-PGQGEGGSDFTLD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: MA-20CCCD3
TELECOMMUNIOATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Foncerrada, Luis
TITLE OF INVENTION: Nematicidal Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.3%; Score 84.5; DE 23.9%; Pred. No. 6.8; tive 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/738,363
FILING DATE: 15-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATE:
FILING DATE: 12-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: BACILLUS THURINGIENSIS INDIVIDUAL ISOLATE: PS17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Sanders, Jay
REGISTRATION NUMBER: 39,355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1289 amino acids
                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09738363 Patent No. US20010010932A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Schnepf, Harry E. Schwab, George E. Payne, Jewel M. Narva, Kenneth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 40 CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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Best Local Similarity 23.98
Matches 56; Conservative
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ORIGINAL SOURCE:
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168 QFDWYEGHQDDIYDMDLNLHAVVKENGQGVWKRPKMYPQEQLNKWRAMDFSKD--FHIYG 225
                                                                103 LEWIPNYVRWIVDGQEVRKIEG---GQVSNLIGIQGLR---FNLWSSESAAWVGQFDE-- 154
                                                                                                         226 CEVNONELIWYVDGVEVARKPNKYWHRPMNVTLSLGLRKPFVKFFDNKNNAINPETDAKA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 24.0%; Pred. No. 4.8;
Matches 56; Conservative 29; Mismatches 85; Indels 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC_compatible
COMPUTER: IBM PC_COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/738,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: E. COli NM522(pMYC 1627) NRRL B-18651.
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/076,137
FILING DATE: 12-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-20CCCD3
TELECOMUNICATION INFORMATION:
TELEFHONE: 352-375-8100
TELEFAX: 352-372-8600
INFORMATION FOR SEQ 1D NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Foncerrada, Luis
TITLE OF INVENTION: Nematicidal Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: BACILLUS THURINGIENSIS INDIVIDUAL ISOLATE: PS17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 15-Dec-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                              LENGTH: 1385 amino acids
                                                                                                                                                       ----SKLPLFQFINWVKVYKYTPG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09738363 Patent No. US20010010932A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Schnepf, Harry E. Schwab, George E. Payne, Jewel M. Narva, Kenneth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 40
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
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                      1180 QTIEIENFDPDK--EYQLV-----FHGQGEG--TVTLEHGEETKYIETHTHHFANFT 1227
                                                                                   HHAVSPAADQAFHTYGLEWIPNYVRWTVDGQEVRKIEGGQVSNLIGIQGLRFNLWSS--E 144
                                                                                                                                                                       145 SAAWVGQFDESKLPLFQFINWVKVYKYTPGQGEGGSDFTLD-------WTDNFDTFD 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -EVLGKNPGSFQSNIITGKAG---AQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                495 TEFYSSRVNTQYSAVHLGCAGNRPEMKLRQMEMEESMFGD--WHDWGVEVFDGQIVFTID 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQEV----RKTEGGQVSNLTG-TQGLRFNLWSSESAAWVGQFDESKLPLFQFINWVKVYK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    553 GKAVTSSGKDVFGNSVTPAAAPLRPAHFKLSEEEYREVIGO-----PWHLILNTM---- 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 SGTVSSMFLYQNGSEIA.----DGRPWVEVD-IEVLGKNPGSFQSNIITGKAGAQKTSEK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 FSGAELYTLEEVQYGKFEARMKMAAAS-----GTVSSMFLYQNGSEIA--DGRPWVEVDI 59
                                                                                                                                                                                                                                                                                      195 GSRWGKGDWTFDGNRVDLTDKNIYSRDGMLI --- LALTRKGQESFNGQVPRDDE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.3%; Score 84; DB 9; Length 714; llarity 22.5%; Pred. No. 3.5; Conservative 36; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 YTPGQGEGGSDFTLDWTDNFDTFDGSRWGKGDWTFDGNRVDLTDKNI 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEC ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 6377
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6377, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OZAKI, AKIO
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Best Local Similarity
Matches 51; Conserva
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RESULT 7

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GENERAL INFORMATION:
APPLICANT: PAGANO.
APPLICANT: PAGANO.
APPLICANT: PAGANO.
APPLICANT: PAGANO.
APPLICANT: PAGANO.
APPLICANTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FRATMENT OF TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
FILE REFERENCE: 5914-090-999
CURRENT PAPLICATION NUMBER: 60/1-07
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR APPLICATION NUMBER: 60/260,179
NUMBER OF SEO ID NOS: 89
SOFTWARE: PAGENTING DAYE: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          659 ETQNDMKTRYGVLGESSASWTSRGVL----ADALVEYRSLVGPVRPT---FYALHFNP-Y 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- TGTQGLRFNLWSSE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 LHWKKVYLKAILRMKQLEDHEAFETSSLIGHSARVYALYYKDGLLCTGSDDLSAKLWDVS 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Shails, Ajay
APPLICANT: Sheiky, Yasir A.W.
APPLICANT: Sheiky, Yasir A.W.
APPLICANT: Shobst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2011-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.3%; Score 83.5; DE Best Local Similarity 22.1%; Pred. No. 2; Matches 30; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Mismatches
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Patent No. US20020061848A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 LEWTPNYVRWTVDGQEVRKTEGGQVSNL-
Sequence 4, Application US/10042417
Patent No. US20020123082A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50; Conservative
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ORGANISM: Homo sapiens
US-10-042-417-4
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Matches 50; Conserv
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Score 83.5; |
Pred. No. 11;
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: Patent No. US20020128166Al

: GENERAL INFORMATION:

: APPLICANT: Henkel KGaA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Bacillus sp. CBS 670.93
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                                                                                                8 SGAELYTLEEVQYG-----
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Best Local Similarity
                              Query Match
Best Local Similarity
Matches 50; Conserv
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US-10-007-693-98
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             -TLDWTDNF 190
                                    50 DGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNY 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 VR------WIYDGQEVRKIEGGQVSNLIGIQGLRFNLWSSESAAWVGQFDESKLPL 159
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| Sequence 118, Application US/09841132
| Patent No. US20020061848A1
| GENERAL INFORMATION:
| APPLICANT: Bhatia, Ajay
| APPLICANT: Shatia, Peter
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
| FILE REFERENCE: 210121.469C8
| CURRENT FILING DATE: 2001-04-23
| NUMBER OF SEQ ID NOS: 599
| SOFTWARE: FastESQ for Windows Version 3.0/4.0
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Patent No. US20020146776a1
GENERAL INFORMATION:
APPLICANT: Braita, Ajay
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121 515C2
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.3%; Score 83.5; 20.4%; Pred. No. 11;
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             160 FQFIN-----WVKVYKYTPGQG----EGGSDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.3%
Best Local Similarity 20.4%
Matches 50; Conservative
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LENGTH: 1531
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US-10-007-693-98
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1342 ETQNDMKTRYGVLGESSASASTSRGVL----ADALVEYRSLVGPVRPT---FYALHFNP-Y 1393
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                                                                                                               --KFEARMKMAAASGTVSSMFL----YQNGSEIA 49
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                                                                                                                                                                                                                                      DGRPWVEVDIEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNY
                                                                                                                                                                                                                                                                                                                                                                                                                    1394 VEVSYASMKFPGFTEQGREARSFEDASLTNITIPLGMKFEL-----AFIKGQFSE----
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Length 1531;
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                                                       Indels
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APPLICANT: Wan Beckhoven, Rudolf F. W. C.
APPLICANT: Wan Beckhoven, Rudolf F. W. C.
APPLICANT: Maurer, Karl-Heinz
APPLICANT: Wanser, Karl-Heinz
APPLICANT: Weiss, Albrecht
APPLICANT: Weiss, Albrecht
APPLICANT: Weiss, Albrecht
APPLICANT: Wom Solingen, Pieter
TITLE REFERENCE: H 1920 A
CURRENT APPLICATION NUMBER: US/09/863,547B
CURRENT FILING DATE: 2002-02-13
PRIOR FILING DATE: 1998-02-27
PRIOR FILING DATE: 1998-02-27
PRIOR FILING DATE: 1996-04-26
PRIOR FILING DATE: 1996-04-28
PRIOR FILING DATE: 1996-04-28
PRIOR FILING DATE: 1995-04-28
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DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
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Pred. No. 4.4;
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                                                       34; Mismatches
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14;
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                                                                                                                                                                                                                                                                                        142 TGDTTQYGSSAALPFRQWVSQGHRMLWLGEPGRIYSELA--ASWLGV-LAVGGFALLWLR 198
                                                                                                                                                                                                                                                                                                                                     64 -KNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQ--AFHTY-GLEWTP------NY 109
                                                                                                                                                                                                                                                                                                                                                                            199 NKKPGRLRKMVRTGGRGRVKTYRRHAALGTVAGLGFVFLTFTGLTWSTYAGSNITDLRTQ 258
                                                                                                                                                                                                                                                                                                                                                                                                                            110 VRWTVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSESAAWVGQFD------ESKLPLFQ 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 FINWVKVYKYTPGQGEGGSDFTLDW--TDNFDTFDGSRWGKGDWTFDG-----NRVDLT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 GSFQSNIITGKAGAQKTSEKHHAVSPAADQ----AFHTYGLEWTPN------YVRW 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 TVDGQEVRKTEGGQVSNLTGTQGLRFNLWSSES------AAWVGQFDESKLPLFQ 161
                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                        63;
                                                                                                                                                                                                                                               14 TLEEVQYGKFEARMKMAAASGTVSSMFLYQNG---SEIADGRPWVEVDIEVLG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 231;
                                                                                                                                                          DB 9; Length 475;
                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                   94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Town wonfeng
APPLICANT: Xu, Wenfeng
APPLICANT: Chen, Zhi
TILEOR INVENTION: Human Cytokine Receptor
FILE REFERENCE: 99-93
CURRENT APPLICATION: Human Cytokine Receptor
FILE REFERENCE: 199-93
CURRENT APPLICATION NUMBER: US/09/728,911
CURRENT APPLICATION NUMBER: US 60/169,049
PRIOR APPLICATION NUMBER: US 60/169,049
PRIOR FILING DATE: 2000-13 60/232,219
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: US 60/232,219
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 360/244,610
SEQ ID NOS: 360/2003 3.0
SEQ ID NOS: 360/2003 3.0
                                                                                                                                                    5.9%; Score 78.5; DF
24.5%; Pred. No. 7;
tive 25; Mismatches
                                                                    ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09728911
Patent No. US20020012669A1
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 6052
LENGTH: 475
                                                                                                                                                        Query Match
Best Local Similarity 24.5%
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-728-911-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 FINWVKVYKYTP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Best Local Simi
Matches 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved TITLE OF INVENTION: in the synthesis of carbohydrates
FILE REFERENCE: BASE-NAE-1332-99-US
CURRENT APPLICATION NUMBER: US/09/734,569
CURRENT FILING DATE: 2001-05-24
PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 181
SOFTWARE: PATENTION NOS: 181
SEQ ID NOS: 18
LENGTH: 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 YGKFEARMKMAA--ASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNPGS---FQSNII 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 6.0%; Score 80; DB 10; Length 156
Best Local Similarity 25.0%; Pred. No. 1.2;
Matches 24; Conservative 19; Mismatches 39; Indels
  278 MDERNL---SWANWSLTHKDESSAALMPGANPTGG-----WTE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 TGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 VDGVGGRE-QQMYLGFDPSAD--FHYYRFRWSKDMV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-4-07
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6052, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                             Sequence 28, Application US/09734569 Patent No. US20020064816A1
                                                                                                                                                                                                                                                                                                                                                     Duwenig, Elke
Schmidt, Ralf-Michael
Reski, Ralf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-734-569-28
                                                                                                                                                                                                                                                                                   Bischoff, Friedrich
Frank, Markus
Freund, Annette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                        Renz, Andreas
Ehrhardt, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NAKAGAWA, SATOSHI
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                                                                                                                                                                                                                                                                      Cirpus, Petra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANDO, SEIKO
                                                                                                                                                                               APPLICANT: Lerchl, Jens
                                                               RESULT 12
US-09-734-569-28
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Search completed: January 9, 2003, 12:14:39 Job time : 7.31481 secs

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January 9, 2003, 12:05:57 ; Search time 25.8333 Seconds (without alignments) 1279.206 Million cell updates/sec
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/ SIDS2/goddata/geneseq/geneseqp-emb1/RA1990.DAT: *
/ SIDS2/goddata/geneseq/geneseqp-emb1/RA1991.DAT: *
/ SIDS2/goddata/geneseq/geneseqp-emb1/RA1991.DAT: *
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/ SIDS2/goddata/geneseq/geneseqp-emb1/RA1995.DAT: *
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1333
1 MVSAKDFSGAELYTLEEVQY.....TRKGQESFNGQVPRDDEPAP 248
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SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS2/gcgdata/geneseqygeneseqp-embl/AA1981.DAT:*
/SIDS2/gcgdata/geneseqygeneseqp-embl/AA1982.DAT:*
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	B. alkalophilus be	Bacillus subtilis	Barley recombinant	Hybrid (1,3-1,4)-p	Thermostable beta-	Heat-stable endo-b	Bacterial lichenas	Bacterial lichenas	Hybrid (1,3-1,4)-p	Lichenase protein.
	ID	AAW93001	AAP95000	AAE07317	AAR06621	AAR03775	AAR05803	ABB76858	ABB76859	AAR06622	AAW37884
	DB	20	10	22	11	11	11	23	23	11	19
	Watch Length DB ID	308	242	214	239	234	237	208	214	237	245
æ (	Match	19.3	18.5	18.3	18.3	17.0	17.0	16.9	16.9	16.5	14.2
	Score	257.5	246.5	244	244	226	226	225	225	220.5	189
+[	No.	1	7	ж	4	2	9	7	80	6	10

Hillen W, Maurer K; WPI; 1999-122161/11. N-PSDB; AAX02912.

(HENK ) HENKEL KGAA.

New Bacillus alkalophilus beta-glucanase protein and gene - useful for removing glucan and/or lichenan from membranes in the brewing industry

Arabidopsis thalia Herbicidally activ Arabidopsis thalia Herbicidally activ Arabidopsis thalia Herbicidally activ Arabidopsis thalia Arabidopsis thalia Herbicidally activ Arabidopsis thalia Herbicidally activ Herbicidally activ Herbicidally activ	Herbicidally activ Clostridium perfri Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Herbicidally activ Arabidopsis thalia Oerskovia beta-1,3 Protein encoded by A. thaliana merist Herbicidally activ Oerskovia xanthine Arabidopsis thalia Oerskovia xanthine Beta-1,3-glucanase Oerskovia xanthine Arabidopsis thalia Arabidopsis thalia	an; membrane;
AAG4846 ABB9373 AAG3246 ABB9145 AAG5211 AAG5211 AAG1864 AAG1864 AAG1864 AAG1864 AAG1864 AAG1864 ABB9316 ABB9316	ABB93104 ABB93104 AAB938654 AAG20347 AAG20346 AAG20349 AAG20328 AAG20328 AAG20328 AAG20328 AAG20328 AAR97362 AAR97362 AAR97362 AAR97362 AAR97362 AAR97362 AAR97362 AAR97363 AAR97363 AAR97363 AAR97363 AAR97363 AAR97363 AAR97363 AAR97363	ALIGNMENTS  in; 308 AA.  y)  icanase protein.  glucan; removal; lichenan;  brewing.  751.
13.8 282 13.9 282 12.9 282 12.9 277 12.9 277 12.7 282 12.7 282 12.7 282 12.7 282 12.7 282 12.7 282		standard; Protein 99 (first entry) philus beta-gluca anase; enzyme; g]; food industry; alkalophilus. 1-Al. 99. 97; 97DE-103275
11 17 11 11 11 11 11 11 11 11 11 11 11 1	23 159 25 150.5 26 150.5 28 150.5 29 150.5 30 150.5 31 149.5 35 149.5 36 147 37 149.5 38 149.5 39 149.5 40 147 41 140.5	RESULT 1 AAM93001 star XX AC AAM93001; XX DT 19-MAY-1999 XX DE B. alkalophil XX W Beta-glucans XM W equipment; f XX CoS Bacillus alka XX PN DE19732751-Al XX PN DE19732751-Al XX PN AC AAM93001; XX

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GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                         AAE07317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
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                                                                                                                   RESULT 3
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                                                                                                                  9
                           This sequence represents a novel beta-glucanase isolated from Bacillus alkalophilus DSM 9956. This enzyme is useful for removing glucan and/or lichenan from membranes and equipment in the food industry, especially
                                                                                                                                                                                    PGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGG 125
                                                                                                                   Gaps
                                                                                                                                   6 DFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The lichenase gene from Bacillus subtilis Y-25 is used for transforming Bacillus hosts so that they show increased lichenase expression. The recombinant lichenase enzyme produced by the transformants is useful in beer production for decomposing beta-
                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                           production; fermentation; barley; beta-glucan; hydrolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant plasmid used in beer prodn. - obtd. by integrating lichenase gene derived from Bacillus subtilis, into vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 242;
                                                                                                                                                                                                              126 QVSNLTGT-QGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYTP 173
                                                                                                                                                                                                                          - TENIPQTPQKIMMNLWPGIGVDGWTGVFDGEDTPVVTEXDWV---RYTP 254
                                                                                               Length
                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.5%; Score 246.5; DB 10; 35.5%; Pred. No. 4e-16; ive 24; Mismatches 74;
                                                                                              DB 20;
                                                                                                                  73;
                                                                                              Score 257.5; DB 2 Pred. No. 4.5e-17;
                                                                                       19.3%; Sco...
36.5%; Pred. No. 4...
4.ve 22; Mismatches
                                                                                                                                                                                                                                                                                AAP95000 standard; Protein; 242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 4; 7pp; Japanese.
        Claim 6; Page 5; 8pp; German.
                                                                                                                                                                                                                                                                                                                                        Bacillus subtilis lichenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                87JP-0224615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87JP-0224615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ASAK ) ASAHI BREWERIES KK
                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                      Local Similarity 36.5
nes 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 18.5
Best Local Similarity 35.5
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis Y-25
                                                         the brewing industry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1989-119863/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glucan from barley
                                                                            308 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAN95000
                                                                                                                                                                                                                                                                                                                                                                                                         JP01067181-A
                                                                                                                                                                                                                                                                                                                                                                                                                                               08-SEP-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-1987;
                                                                                                                                                                                                                                                                                                                      12-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-1989
                                                                             Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                               Query Match
                                                                                                       Best Loca
Matches
                                                                                                                                                      96
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                                                                                                                                                                                                                                 209
                                                                                                                                                                                                                                                                                                                                                           Beer
                                                                                                                                                                                                                                                                      AAP95000
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The present invention relates to a food stuff comprising barley feed and transgenic barley malt where the transgenic barley malt comprises a recombinant carbohydrate degrading enzyme comprising a (1,3:1,4)-beta glucanase. The food stuff is useful to feed animal, preferably chickens Barley is cheaper than corn, the principal foodstuff of chickens. Chickens cannot efficiently utilise barley as an energy source as they do not possess a gut enzyme that depolymentises beta-D-glucan, major carbohydrate present in the barley endosperm. The invention provides a barley based foodstuff which comprises a recombinant carbohydrate present in the barley endosperm: The invention provides a degrading enzyme improving the nutritional value of the foodstuff. The present sequence is barley recombinant, thermostable (1,3-1,4)-beta-glucanase enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNKFDCGENRSVQTYGYGYGYEYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDIEFL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barley; transgenic barley malt; carbohydrate degrading enzyme; chicke
(1,3-1,4)-beta-glucanase; nutritional value; foodstuff; thermostable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New barley based foodstuff for animals, i.e. chicken comprising recombinant carbohydrate degrading enzyme (1,3-1,4)-beta-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                              Barley recombinant, thermostable (1,3-1,4)-beta-glucanase enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
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EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                   |: ||: :||: |
196 ATNQIPTTPGK--IMMNLWNGTGVDEWLGSYNGVN-PLYAHYDWVRYTK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.3%; Score 244; DB 22;
35.5%; Pred. No. 5.9e-16;
11ve 26; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNIW ) UNIV WASHINGTON STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huang J, Horvath H;
                                                                                                                                                                                                                                            Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 37-38; 43pp; English.
                                                                                                                                                                                                                                     AAE07317 standard; Protein; 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-FEB-2001; 2001WO-US04222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-FEB-2000; 2000US-0181473.
09-NOV-2000; 2000US-0247126.
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Matches 61, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-497082/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Von Wettstein D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hordeum vulgare.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200159141-A2.
                                                                                                                                                                                                                                                                                                                                                                           06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55
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Gaps

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74; Indels

3 SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL 62

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88DD-0315706
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                                                                                                                                                                                                                    Thermostable beta-glucanase
                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-NOV-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fig 1; ; 9pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1990-067913/10.
N-PSDB; AAQ03519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 AA;
                                                                                                                                                                                                                                                                                                 Bacillus macerans,
                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAY-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAY-1988;
                                                                                                                                                                              31-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59;
                                                                                                                                                                                                                                                                                                                                                                                27-SEP-1989
                                                                                                                                                                                                                                                                                                                                        DD272102-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borriss R;
                                                                                                                                       AAR03775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR05803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29
193
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                                                          RESULT 5
                                                                            AAR03775
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&
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIAIJGRPWVEVDIEVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This hybrid protein is encoded by the beta-glucanase-H1 gene. Following processing of the signal peptide the mature protein is produced, comprising the amino terminal of the amylolique-faciens beta-glucanase and the carboxyl-terminal half of the B.macerans beta-glucanase. This hybrid protein is thermostable and hydrolyses beta-glycosidic linkages in (1,3-1,4) beta-glucans. Reducing sugars are obtd. at high temps. and thus this enzyme can be used in the mfr. of food prods., esp. beer and animal feed (eg for feeding poultry). See also AAQ05833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vonwettstein D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New thermostable (1,3-1,4)-beta-glucanase - prepd. using hybrid gene obtd. using Bacillus amyloliquefaciens and B.macerans genes
                                                                                                                                                                                                                                                                                                                                                                                                                     of beta-amyloliquefaciens
                                                                                                                                                                                                                                                                                               pre-beta-glucanase; glucans; beer; animal feed; poultry.
123 EGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKYYKYT 172
                        123 EGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.3%; Score 244; DB 11; Length 239; 35.5%; Pred. No. 6.9e-16; ive 26; Mismatches 69; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        133..236
/label=carboxyl-terminal of B.macerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olsen O,
                                                                                                                                                                                                                                                                                                                                      Bacillus amyloliquefaciens, Bacillus macerans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thomsen KK,
                                                                                                                                                                                                                                                                                                                                                                                                     1..129
/label-amino terminal
                                                                                                                                                                                                                                                         Hybrid (1,3-1,4)-pre-beta-glucanase.
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; page 26; 84pp; English.
                                                                                                                                     AAR06621 standard; protein; 239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CARL-) CARLSBERG A/S.
(DEAK ) AKAD WISSENSCHAFT DDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90WO-DK00044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89DK-0003848
89DD-0325800
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                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 18.3
Best Local Similarity 35.5
Matches 61; Conservative
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N-PSDB; AAQ05832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-FEB-1990;
                                                                                                                                                                                                                  09-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9009436-A.
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16-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-AUG-1990
                                                                                                                                                                              AAR06621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                 Hybrid
                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
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                                     168
                                                                                               RESULT 4
                                                                                                                    AAR06621
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GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
---ATANIPSTPGKIMMNLWAGTGVDDWLGSYNGAN-PLYAEYDWV---KYT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 VSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The gene encoding Bacillus macerans thermostable beta-glucanase is expressed in Bacillus subtilis. The enzyme is useful for lowering the viscosity of brewing mashes and in the production of feedstuff.
                                                                                                                                                                                                                                                                                                                                                   Thermostable beta-glucanase; ss; Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.0%; Score 226; DB 11;
35.1%; Pred. No. 4.1e-14;
tive 23; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermostable beta-glucanase production using Bacillus subtilis transformed with macerans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heat-stable endo-beta-1,3-1,4-glucanase.
                                                                                                                                                  AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR05803 standard; protein; 237 AA
                                                                                                                                            AAR03775 standard; protein; 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DEAK ) AKAD WISSENSCHAFT DDR
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(CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
                                      WPI; 2002-217195/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacterial lichenase
                    Rodriguez Munoz V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-217195/27
N-PSDB; ABL53375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rodriguez Munoz V,
                                                                                                                                                                           208 AA;
                                               N-PSDB; ABL53374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200212511-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-2002
                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    ABB76859;
                                                                                                                                                                                                                                                                                             115
                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                RESULT 8
                                                                                                                                                                                                                                                                                                                                                                          ABB76859
 qq
                                                                                                                                                                                                                                                                                           Dp
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                                                                                                                                                                                                                                          The corresp, gene and the plant promoter region are inserted into an expression vector and used to transform barley cells. The transformants are used to regenerate barley plants which are useful in brewing. This protein accumulates in the ripe (but ungerminated) seeds. The proportion of these to malted seeds is increased therefore, without an unacceptable increase in viscosity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soil bacterium; enzyme; lichenase; endo-1,3/1,4-beta-glucanase; brewing
                                                                                                                                                                                                                                                                                                                                                                                  GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                         139 TKVQFNYYTNGVGGH---EKVISLGFDASKGFHTYAFDWQPGYIKWYVDG-VLKHT---A 191
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                       FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                                                                                                                                                                   Prepn. of barley plants expressing heat stable beta-glucanase - by transforming cells with appropriate vector then regeneration giving seeds useful in brewing without conversion to malt.
                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                / Match 17.0%; Score 226; DB 11; Length 237; Local Similarity 35.1%; Pred. No. 4.2e-14; nes 59; Conservative 23; Mismatches 70; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 VSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYKYT 172
                                                                                                                                     Baumlein H;
Endo-beta-1,3-1,4-glucanase; barley; brewing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB76858 standard; Protein; 208 AA
                                                                                                                                    Mendel R-R,
                                                                                                                  (DEAK ) AKAD WISSENSCHAFT DDR
                                                                           88DD-0320082
                                                                                               88DD-0320082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JUL-2001; 2001WO-ES00303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-2000; 2000ES-0001922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                         Disclosure; ; p; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacterial lichenase #1
                                                                                                                                     Borriss R, Wobus U,
                                                                                                                                                      1990-210631/28.
                                                                                                                                                                                                                                                                                                               237 AA;
                   Bacillus macerans
                                                                                                                                                                 N-PSDB; AAQ05167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200212511-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                           23-SEP-1988;
                                                                                              23-SEP-1988;
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                                                        31-JAN-1990
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                                     DD275704-A
                                                                                                                                                                                                                                                                                                                Sednence
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Matches
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Producing nucleic acid encoding lichenase, useful for producing enzymes for improving filtration in brewing, comprises isolating the nucleic acid from soil bacteria -
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                                                                                                                                                                                                                                                                                                                                                                             au
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a protein sequence from a soil bacterium for an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVU 62
                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a protein sequence from a soil bacterium fearyme with lichenase/endo-1,3/1,4-beta-glucanase (E.C. 3.2.1.73) activity. The enzyme is useful in brewing and for degrading beta-glucanases that cause problems during filtration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 16.9%; Score 225; DB 23; Best Local Similarity 36.2%; Pred. No. 4.3e-14; Matches 55; Conservative 21; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 EGGOVSNLTGTOGLRFNLWSSESA-AWVGOFD 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 ATTOIPAAPGK--IMMNLWNGTGVDDWLGSYN 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                   Claim 18; Page 18-19; 27pp; Spanish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page 21-22; 27pp; Spanish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
Perez Mellado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perez Mellado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB76859 standard; Protein; 214
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WO9814595-A1
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                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW37884;
                                                           AAQ05833
                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
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        22 22 X 88
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/label-amino-terminal half of B.macerans beta-glucanase
131..234
/label-carboxyl-terminal half of B.amyloliquefaciens
                                                                                                                                                                                                                                                                                          63 SYNKFDCGENRSVQTYGYGLYEVRMKPAKNTGIVSSFFTYTGPTE---GTPWDEIDIEFL 119
                                                                                                                                                                                                                                                                                                                                                                                                GKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVFWTVDGQEVRKT 122
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vonwettstein D;
                                                                                                                                                                                                                                                          3 SAKDFSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVL
enzyme with lichenase/endo-1,3/1,4-beta-glucanase (E.C. 3.2.1.73) activity. The enzyme is useful in brewing and for degrading beta-glucanases that cause problems during filtration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New thermostable (1,3-1,4)-beta-glucanase - prepd. using hybrid gene obtd. using Bacillus amyloliquefaciens and B.macerans genes
                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hybrid pre-beta-glucanase; glucans; beer; animal feed; poultry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This hybrid protein is encoded by the beta-glucanase-H2 gene. Following processing of the signal peptide the mature protein is produced, comprising the amino terminus of the B.macerans beta-glucanase and the carboxyl-terminal half of the B.amylo-liquefaciens beta-glucanese. This hybrid protein is thermostable and hydrolyses beta-glycosidic linkages in (1,3-1,4)-beta-glucans. Reducing sugars are obtd. at high temps, and
                                                                                                                                                            Length 214;
                                                                                                                                                                                                               66; Incels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olsen O,
                                                                                                                                                      16.9%; Score 225; DB 23;
36.2%; Pred. No. 4.5e-14;
ive 21; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus amyloliquefaciens, Bacillus macerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1 :: | 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGGQVSNLTGTQGLRFNLWSSESA-AWVGQFD 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R, Hofemeister J, Thomsen KK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hybrid (1,3-1,4)-pre-beta-glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR06622 standard; protein; 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CARL-) CARLSBERG A/S.
(DEAK ) AKAD WISSENSCHAFT DDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90WO-DK00044
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89DD-0325800.
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                                                                                                                                                                                 Local Similarity 36.2 nes 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1990-275129/36.
                                                                                                        214 AA;
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16-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JAN-1991
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                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR06622;
                                                                                                                                                            Query Match
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Matches
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                                                                                                                                                                                  67 GSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQ 126
                                                                                                                                                                                                                                                    139 TKVQFNYYTNGAG---NHEKFADLGFDAANAYHTYAFDWQPNSIKWYVDGQ-LKHTATTQ 194
                                                                                                                                                               7 FSGAELYTLEEVQYGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lichenase; licA; fungus; enzyme; beta-1,4-glucan bond hydrolysation; beta-1,3-linked glucan bond; grain-containing feed; grain treatment; nutrient availability; brewing; fermentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated lichenase protein - is obtained from Orpinomyces PC-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used for treatment of grain to improve feeds or to improve brewing
                                                                                                DB 11; Length 237;
                 See also
prods.,
                                                                                                                                Indels
                                                                                                                                                                                                                                                                                              127 VSNLTGTQGLRFNLWSSESA-AWVGQFDESKLPLFQFINWVKVYK 170
                                                                                                                                                                                                                                                                                                                     16.5%; Score 220.5; DB 11;
33.9%; Pred. No. 1.5e-13;
... wtematches 75;
thus this enzyme can be used in the mfr. of food beer and animal feed (e.g.for feeding poultry).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "mature lichenase"
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/note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 24-25; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                AAW37884 standard; Protein; 245
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                                                                                                       when, similaric, watches 56; Conservative
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                                                             237 AA;
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990S-013724
990S-0137502
990S-0139454
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990S-0140354.
990S-0140695.
990S-0140823.
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99US-0142154.
99US-0142055.
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990S-0145145
990S-0145218
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990S-0145913
990S-0145913
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   8
                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                   59 IEVLGKNPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQE 118
                                                                                            of grain (e.g. barley or wheat) in the brewing and fermentation industries to increase carbon substrate availability and to maximise production of desired products.
                                                                    Gaps
                                                                                  5 KDFSGAELYTLEEVQ-----YGKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVD 58
                                                 14.2%; Score 189; DB 19; Length 245; 32.9%; Pred. No. 2e-10; ive 16; Mismatches 76; Indels 22;
                                                                                                                                                    119 VRKTEGGQVSNLTGTQG-LRFNLWSSESA-AWVGQFDESKLPLFQFINWV 166
                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 61207
                                                                                                                                                                                                              AAG48467 standard; Protein; 282 AA
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990S-0123180
990S-0125788
990S-0125788
990S-0126765
990S-0126734
990S-0128234
990S-0128234
990S-013884
990S-0130077
990S-0131449
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990S-0132486
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990S-0134219.
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990S-0134768.
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                                                                                                                                                                                                                                                (first entry)
                                                Query Match
Best Local Similarity 32.9
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
                                 245 AA;
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25-MAR-1999;
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06-APR-1999;
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06-MAY-1999;
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26-OCT-1999;
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29-SEP-19
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15-SEP-19
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08-0CT-19
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13-0CT-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sednences
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                            2 VSAKDFSGAELYTLEEVQYGKFEARMKMAA--ASGTVSSMFLYQNGSEIADGRPWVEVDI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                          QEVRKTEGGQVSNL - -TGTQGLRF - - NLWSSESAAWVG - - - QFDESKLPLFQFINWVKVY
                                                                                                                                                                                                                                                                                                                                                                              EVLGK - - - NPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDG
                                                                                                                                                                                                                                                                                                                                                                                                            | || :| :| | | : |:| || EFLGNISGHPYTLHTNVYT-KGTGDKEQQFHLWFDPTVD--FHTYCIIWNPQRVIFTIDG
                                                                                                                                                                                                                                24;
                                                                                                                                                                            Length 282;
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                                                                                                                                                                                                                                Indels
                                                                                                                                                                            13.8%; Score 184; DB 21; 27.6%; Pred. No. 7.8e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 ACVWSNGKSSCSANSSWFTQVLDFKGKNRVKWAQ 258
                                                                                                                                                                                                                                Mismatches
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99US-0161360.
99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
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  26-0CT-1999;
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990S - 0.13918.9

990S - 0.140354.

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990S - 0.140695.

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990S - 0.14218.7

990S - 0.142154.

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99US-0145086.
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23-JUL-1999;
23-JUL-1999;
23-JUL-1999;
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27-JUL-1999;
27-JUL-1999;
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       6
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                                                                                                                                                                                                                                                                                                                                            117 QEVRKTEGGQVSNL--TGTQGLRF--NLWSSESAAWVG---QFDESKLPLFQFINWVKVY 169
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                   2 VSAKDFSGAELYTLEEVQYGKFEARMKMAA--ASGTVSSMFLYQNGSEIADGRPWVEVDI 59
                                                / Match 13.8%; Score 184; DB 23; Length 282; Local Similarity 27.6%; Pred. No. 7.8e-10; les 59; Conservative 33; Mismatches 98; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thallana protein fragment SEQ ID NO: 39167.
                                                                                                                                                                                                                                                                                                                                                                                                                                             170 KYTPGQGEGGSDFTLDWTDNFDTFDGS---RWGK 200
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  282 AA;
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26-OCT-1999;
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99US-0161359
99US-0145951
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17-AUG-1999;
          02-AUG-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGGQVSNL--TGTQGLRF--NLWSSESAAWVG---QFDESKLPLFQFINWVKVYKYTPGQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- NPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                              GEGGSDFTLDWTDNFDTFDGSRWGKGDWTFDGNRVDLTDKNIYSRDGMLILALTRKGQES
                                                                                                                                                                                                                               58;
                                                                                                                                                                     Length 282;
                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                  12.9%; Score 172; DB 21; 25.9%; Pred. No. 1.2e-08; ive 34; Mismatches 88;
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990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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                                                                                                                                                                        Query Match
Best Local Similarity
Matches 63; Conserv
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25-MAY-1999;
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 12;
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sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                        EGGQVSNL--TGTQGLRF--NLWSSESAAWVG---QFDESKLPLFQFINWVKVYKYTPGQ 175
                                                                                                    65 --NPGSFQSNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKT 122
                                                                                                                                                                                                    176 GEGGSDFTLDWTDNFDTFDGSRWGKGDWTFDGNRVDLTDKNIYSRDGMLILALTRKGQES 235
                                                                                                                                                                                                                 Gaps
                                                                                        8 SGAELYTLEEVQYGKFEARMKMAA--ASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGK- 64
                                                                                                                                                                           58;
                                                    12.9%; Score 172; DB 23; Length 282; 25.9%; Pred. No. 1.2e-08; ive 34; Mismatches 88; Indels 5
                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thallana protein fragment SEQ ID NO: 66212.
                                                                                                                                                                                                                                                                                                        AAG52114 standard; Protein; 277 AA
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99US-0128714.
99US-0129845.
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990S-0132048.
990S-0132407.
990S-0132484.
99US-0132485.
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99US-0123180.
99US-0123548.
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99US-0126264.
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99US-0130449.
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99US-0130891.
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                                                              Best Local Similarity 25.9%
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                                    282 AA;
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05-MAR-1999

23-MAR-1999

25-MAR-1999

01-APR-1999

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25-APR-1999

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PR 22-7UL-1999; 99US-0145192.
PR 23-7UL-1999; 99US-0145145.
PR 23-7UL-1999; 99US-0145214.
PR 23-7UL-1999; 99US-0145214.
PR 23-7UL-1999; 99US-0145214.
PR 23-7UL-1999; 99US-0145214.
PR 27-7UL-1999; 99US-0145218.
PR 27-7UL-1999; 99US-0145918.
PR 27-7UL-1999; 99US-0145918.
PR 02-MC-1999; 99US-0145918.
PR 02-MC-1999; 99US-0145918.
PR 02-MC-1999; 99US-0145918.
PR 03-MC-1999; 99US-0144391.
PR 03-MC-1999; 99US-0144391.
PR 13-MC-1999; 99US-0144392.
PR 13-MC-1999; 99US-0144311.
PR 13-MC-1999; 99US-0144311.
PR 13-MC-1999; 99US-0149173.
PR 13-MC-1999; 99US-0149173.
PR 13-MC-1999; 99US-0149173.
PR 13-MC-1999; 99US-0149173.
PR 25-MC-1999; 99US-0149173.
PR 27-MC-1999; 99US-0151066.
PR 27-MC-1999; 99US-0151066.
PR 27-MC-1999; 99US-0151066.
PR 27-MC-1999; 99US-015108.
PR 27-MC-1999; 99US-
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                                                                                                                                                                                  41;
                                                                                                                                                            12.9%; Score 171.5; DB 21; Length 277; 27.0%; Pred. No. 1.3e-08; ive 32; Mismatches 70; Indels 41;
                                                                                                                                                                                 70; Indels
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99US-0160815.
99US-0160980.
99US-0160981.
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99US-0161405.
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99US-0161359.
99US-0161360.
99US-0161361.
99US-0161920.
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                                                                                                                                                                      Local Similarity 27.0 les 53; Conservative
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Job time: 27.8333 secs
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
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Matches
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9, 2003, 12:04:12 ; Search time 11.7431 Seconds
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1439
1 MYSAKDFSGAELYTLEEVQY......PNSSSVDKLAAALEHHHHHH 267
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Sequence:
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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

Total number of hits satisfying chosen parameters: 263044 seqs, 70945482 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pending\_Patents\_AA\_New:\*

1: /cgn2\_6/ptcdata/2/paa/US06\_NEW\_COMB.pep:\*

2: /cgn2\_6/ptcdata/2/paa/US06\_NEW\_COMB.pep:\*

3: /cgn2\_6/ptcdata/2/paa/US07\_NEW\_COMB.pep:\*

4: /cgn2\_6/ptcdata/2/paa/US08\_NEW\_COMB.pep:\*

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6: /cgn2\_6/ptcdata/2/paa/US08\_NEW\_COMB.pep:\*

7: /cgn2\_6/ptcdata/2/paa/US08\_NEW\_COMB.pep:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 3, Appli		833	Sequence 83340, A			Sequence 10, Appl	8334	83343,		83344,	83342,		59,	4	4	48,	49,	50,	51,	Sequence 52, Appl	53,	54,	26,	58,	Sequence 122, App
ID	US-10-294-561-3	US-10-010-160-68		US-09-724-676A-83340	-09-724	-09-724		7	US-09-724-676A-83343	2-60	7-60	US-09-724-676-83342	19-724-	-141 - 5	9-424-	US-10-141-531-47	0-141-531-4	0 - 141 -	0-141-531-5	0 - 141 - 531 - 5	US-10-141-531-52	.0-141-531-	10-141-5	0 - 141 - 531	US-10-141-531-58	US-10-114-104A-122
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Score	116.5	113	104.5	104.5	103.5	103.5	100.5	99.5	99.5	98.5	98.5	97.5	97.5	97	94	92	85	92	92	92	92	92	92	92	92	06
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RESULT 2
US-10-010-160-68
US-10-010-160-68, Application US/10010160
; GENERAL INFORMATION:

Sequence 121, App	Sequence 2151, Ap	Sequence 4346, Ap	Sequence 60984, A	Sequence 60984, A	Sequence 9, Appli		1,	Sequence 1219, Ap	Sequence 3, Appli	Sequence 1920, Ap	Sequence 1920, Ap		Sequence 1264, Ap	Sequence 1280, Ap	Sequence 1280, Ap	Sequence 8, Appli	Sequence 14093, A	Sequence 861, App
US-10-114-104A-121	US-10-276-774-2151	US-10-092-411A-4346	US-09-724-676-60984	US-09-724-676A-60984	US-09-917-384A-9	US-09-917-384A-5	US-09-917-384A-1	US-10-276-781-1219	PCT-US02-33165-3	PCT-US02-36496-1920	US-10-293-418-1920	PCT-US02-36496-1264	US-10-293-418-1264	PCT-US02-36496-1280	US-10-293-418-1280	US-09-455-294A-8	US-10-203-138A-14093	PCT-US02-36496-861
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398	438	444	486	486	638	640	1121	1125	261	246	246	246	246	250	250	634	209	248
6.3	0.9	0.9	5.8	5.8	5.8	2.8	5.8	5.8	5.7	9.6	5.6	9.6	5.6	2.6	9.6	5.6	5.5	5.5
90	86.5	86.5	83.5	83.5	83.5	83.5	83.5	83.5	82.5	81	81	80.5	80.5	80.5	80.5	80	78.5	78.5
27	28	53	30	1	32	33	34	35	36	37	88	39	01	Ţ	12	m	4	5

## ALIGNMENTS

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Selkagaku Corporation
TITLE OF INVENTION: (1-3)-Beta-D-Glucan Binding Domain Protein, Measuring Method U
TITLE OF INVENTION: Substance And Assay Kit
FILLE REFRENCE: 072918
CURRENT APPLICATION NUMBER: US/10/294,561
PRIOR APPLICATION NUMBER: JP 2001-351943
PRIOR FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
LENGTH: 673
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                                                                                                                                                                                                                                                                                                                                                                                                                                        291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 FHTYGLEWIPNYVRWIVDGQEV--RKIEGGQVSNLIGIQGLRFNLWSSESAA----WVGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 GRPWVEVDIEVLGKNPGSFQSNIITGK-AGAQKTSEKHHAVSPAADQA---
                                                                                                                                                                                                                                                                                                                                           Query Match 8.1%; Score 116.5; DB 6; Best Local Similarity 22.8%; Pred. No. 0.018; Matches 61; Conservative 43; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : : |:| | 292 AFLQQ--WSYSGNENQQFDFEHLENNVY 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 SRWGKGDWTFDGNR-----VDLTDKNIY 218
                                                                                                                                                                                                                                                                                  ; ORGANISM: Tachypleus tridentatus US-10-294-561-3
US-10-294-561-3
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232 GQESFNGQVPRDDEPAPNSSSVDKLAAA 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 21;
APPLICANT: Rosey, Everett L.
APPLICANT: Strugnell, Richard A.
APPLICANT: Strugnell, Richard A.
APPLICANT: Strugnell, Richard A.
APPLICANT: King, Kendall W.
TITLE OF INVENTION: NOVEL THERAPEUTIC COMPOSITIONS FOR
CURRENT APPLICATION NUMBER: US/10/01,160
CURRENT APPLICATION NUMBER: W10/11-09
PRIOR FILING DATE: 2000-11-10
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 68
SEQ ID NOS: 68
SEQ ID NO 68
LENGTH: 21
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTLE OF INVENTION: Variants of alternative splicing TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION NUMBER: US/09/724,676 CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222 SOFTWARE: Patentin version 3.2 SEQ ID NO 83340 LENGTH: 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 113; DB 6; 1
Pred. No. 0.00036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.9%; Sc
Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 PNSSSVDKLAAALEHHHHHH 267
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                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Peptide US-10-010-160-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 18.9
Matches 62; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 SNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNL 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 KVYKYTPGQ-----GEGGSDFTLDWTDNFDTFDGSRWGKGDWTF-DGNR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1510;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 83341, Application US/09724676; GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILER REFERENCE: 129181.4 Compugen
CURRENT APPLICANTON NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222; SOFTWARE: Patentin version 3.2
SEQ ID NO 83341
LENGTH: 1554
                                                                                                                                                                  APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.3%; Score 104.5; DB 5;
18.9%; Pred. No. 0.68;
tive 47; Mismatches 106;
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-----GAILEFDKPEKLLSRKDSVFAS 1504
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                                                                                                                    Sequence 83340, Application US/09724676A GENERAL INFORMATION:
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Matches 62; Conservative
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US-09-724-676A-83340
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US-09-724-676-83341
                                                                                            US-09-724-676A-83340
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US-09-724-676-83341
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                                                          71 SNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNL
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| |: | :| :| :| :| :| 1210 LTIRAFRYEARFQQKLLEYTDSNNIASLFL-----TAAANRWLEVRMEYIG-
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                            167 KVYKYTPGQ------GEGGSDFTLDWTDNFDTFDGSRWG 199
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Best Local Similarity 20.8%; Pred. No. 0.88;
Matches 46; Conservative 36; Mismatches
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APPLICANT: Bannon, Gary A.
APPLICANT: Bannon, Michael J.
APPLICANT: Sampson, Hugh
APPLICANT: Sosin, Howard
TITLE OF INVENTION: Peptide Antigens
FILE REFERENCE: 2002834-0004
CURRENT APPLICATION NUMBER: US/09/455,294A
CURRENT FILING DATE: 1996-09-23
PRIOR PILING DATE: 1996-09-23
PRIOR APPLICATION NUMBER: 08/717,933
PRIOR FILING DATE: 1996-09-23
PRIOR APPLICATION NUMBER: 09/141,220
PRIOR APPLICATION NUMBER: 09/141,220
PRIOR APPLICATION NUMBER: 09/141,220
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Sequence 10, Application US/09455294A
GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-09-724-676A-83341
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US-09-724-676A-83341
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1315 HGLLKTEAESYEGLLGERLRERGGEESKEECVWVGGHKGAWGWGGTFGYSCGPCLVLSPA 1374
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 100.5; DB 5;
Pred. No. 0.38;
4; Mismatches 12;
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PRIOR APPLICATE...

PRIOR PILING DATE: 1998-U2-1,

PRIOR PELLING DATE: 1998-02-1,

PRIOR PELLING DATE: 1998-02-13,

PRIOR PELLING DATE: 1998-02-13,

PRIOR PELLING DATE: 1998-02-13,

PRIOR PELLING DATE: 1998-01-13,

PRIOR PELLING DATE: 1998-01-31,

NUMBER OF SEQ ID NOS: 110

SOFTWARE: PATENTIN Ver. 2.1
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Best Local Similarity 54.1%
Matches 20; Conservative
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ORGANISM: Homo sapiens
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US-09-724-676A-83344
Query Match
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Matches 5
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                                                                                                            Sequence 83343, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 83343
LENGTH: 1558
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GENERAL INFORMATION:
APPLICANT: COmpugen LTD
FILE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 83344
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US-09-724-676A-83343
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ORGANISM: Homo sapiens
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ORGANISM:
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                                                                                                                                                                                                 71 SNIITGKAGAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNL 130
                                                                                                                                                                                                                                                                                                                                                                                                  -----QFDESKLPLFQFINWVKVYKYTPGQ------GE 177
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                                                      Gaps
                                                                                                 12 LYTLEEVQY-GKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNPGSFO 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 LYTLEEVQY-GKFEARMKMAAASGTVSSMFLYQNGSEIADGRPWVEVDIEVLGKNPGSFQ 70
                                                                                                                                                                                                                                                                                                   131 TGT-----QGL-----RFNLWSSESAAWVG-------QGL
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                                                   93;
; DB 5; Length 1602; 2.6;
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                                                   Indels
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Sequence 83344, Application US/09724676A

SENERAL INFORMATION:
APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT APPLICATION NUMBER: US/09/724,676A

NUMBER OF SEQ ID NOS: 97222

SEQ ID NOS: 97222

SEQ ID NOS: 93344
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                                                85;
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                                              33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Mismatches
6.8%; Score 98.5;
19.5%; Pred. No. 2.6
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Sequence 83342, Application US/09724676;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1431 GKSSFSLAFFRMVDTFEGQLEG 1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGSDFTLDWTDNFDTFDGSRWG 199
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                         1 Similarity 19.59 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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DB 6;
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APPLICANT: KIPRIYANOV, SERGEY
APPLICANT: MOLDENHAUER, GERHBARD
APPLICANT: MOLDENHAUER, GERHBARD
APPLICANT: DEUTSCHES KREBSFORSCHUNGSZEUTRUM
TITLE OF INVENTION: MUTATED OKT3 ANTIBODY
FILE REFERENCE: 035280047US00
CURRENT APPLICATION NUMBER: US09/424,705B
CURRENT FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/DE98/01409
PRIOR FILING DATE: 1998-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.7%; Score 97; DB (20.7%; Pred. No. 0.71; Live 30; Mismatches
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; GENERAL INFORMATION:
                               ; FEATURE:
; OTHER INFORMATION: synthetic
US-10-141-531-59
      178 GGSDFTLDWTDNFDTFDG 195
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Best Local Similarity 20.7%
Matches 56; Conservative
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US-09-424-705B-4
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                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                   93;
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                                                                                                                                                                                                                                                                   82; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION WUMBER: US/09/724,676A CURRENT APPLICATION WUMBER: US/09/724,676A NUMBER OF SEQ ID NOS: 97222 SOFTWARE: Patentin version 3.2 SEQ ID NO 83342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82;
                                                                                                                                                                                                                             DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 TGT-----QGL-----RFNLWSSESAAWG-----
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Best Local Similarity 19.4%; Pred. No. 3.3;
Matches 50; Conservative 33; Mismatches
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6.8%; Score 97.5; D
Best Local Similarity 19.4%; Pred. No. 3.3;
Matches 50; Conservative 33; Mismatches
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FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 83342
LENGTH: 1629
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; ORGANISM: Homo sapiens
US-09-724-676A-83342
                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-83342
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US-09-724-676A-83342
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APPLICANT: Dalmia, -
APPLICANT: del Val, Greg
APPLICANT: del Val, Greg
APPLICANT: Desjarlais, John R.
APPLICANT: Desjarlais, John R.
APPLICANT: Luginbulh, Peter
APPLICANT: Luginbulh, Peter
APPLICANT: Luginbulh, Desen
APPLICANT: Muchal, Umesh
TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
FILE PEFERENCE: A-7147-2/FRF/RMS/FMK
CURRENT APPLICATION NUMBER: US, 00/370, 609
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
SPRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAQKTSEKHHAVSPAADQAFHTYGLEWTPNYVRWTVDGQEVRKTEGGQVSNLTGTQGLRF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 RALSNPKIDVIMNSSVVEAYGDGERDVLGG---LKVKNVVTGDVSDLKVSGLFFAIGHEP 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 AIGHEPATKFLDGGVDSAMEEANFLT-----KY-----GSKVYIIHWVDAFGASKIMQQ 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           392 ATKFLDGGVELDSDGYVVTKPGTTQTSVPGVFAAGDVQDKKYRQAITAAGTGCMAALDAE 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 NFD--TFDGSRWGKGDWTFDGNRVDLTDKNIYSRDGMLILALTRKGQESFNGQVPRDDEP 246
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--------KLEIKRADAA 268
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                                                                                                                                                                                                                                                                                                                                                                           101 YGLEWTPNYVRWTVDGQEVRKTEGGQV----SNLTGTQGLR--FNLWSSESAAWVGQF 152
                                                                                                                                                                                        91; Indels 124; Gaps
                                                                                                                                                                                                                           25 ARMKMAAAASGTVSSMFLYQNGSEIADGRP----------------WVE----VDI 59
                                                                                                                                                                                                                                                    Query Match 6.5%; Score 94; DB 5; Length 290; Best Local Similarity 20.4%; Pred. No. 0.67; Matches 66; Conservative 43; Mismatches 91; Indels
: NUMBER OF SEQ ID NOS: 11
; SOFWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 290
; TYPE: PRT
ORCANISM: HOMO sapiens
US-09-424-705B-4
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Search completed: January 9, 2003, 12:14:13 Job time : 13.7431 secs